

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

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 aacctgtca gcctggacgc ctacgtgttc aacaccgaag cccacctct 2100

Asp	His	Trp	Lys	Ala 110	Leu	Ala	Phe	Arg	Leu 115	Glu	Glu	Glu	Gln	Lys 120
Met	Arg	Pro	Glu	Ile 125	Ala	Gly	Leu	Lys	Pro 130	Ala	Asn	Pro	Pro	Val 135
Leu	Pro	Ala	Pro	Gln 140	Lys	Ala	Asp	Thr	Asp 145	Pro	Glu	Asn	Leu	Pro 150
Glu	Ile	Ser	Ser	Gln 155	Lys	Thr	Gln	Arg	His 160	Ile	Gln	Arg	Gly	Pro 165
Pro	His	Leu	Gln	Ile 170	Arg	Pro	Pro	Ser	Gln 175	Asp	Leu	Lys	Asp	Gly 180
Thr	Gln	Glu	Glu	Ala 185	Thr	Lys	Arg	Gln	Glu 190	Ala	Pro	Val	Asp	Pro 195
Arg	Pro	Glu	Gly	Asp 200	Pro	Gln	Arg	Thr	Val 205	Ile	Ser	Trp	Arg	Gly 210
Ala	Val	Ile	Glu	Pro 215	Glu	Gln	Gly	Thr	Glu 220	Leu	Pro	Ser	Arg	Arg 225
Ala	Glu	Val	Pro	Thr 230	Lys	Pro	Pro	Leu	Pro 235	Pro	Ala	Arg	Thr	Gln 240
Gly	Thr	Pro	Val	His 245	Leu	Asn	Tyr	Arg	Gln 250	Lys	Gly	Val	Ile	Asp 255
Val	Phe	Leu	His	Ala 260	Trp	Lys	Gly	Tyr	Arg 265	Lys	Phe	Ala	Trp	Gly 270
His	Asp	Glu	Leu	Lys 275	Pro	Val	Ser	Arg	Ser 280	Phe	Ser	Glu	Trp	Phe 285
Gly	Leu	Gly	Leu	Thr 290	Leu	Ile	Asp	Ala	Leu 295	Asp	Thr	Met	Trp	Ile 300
Leu	Gly	Leu	Arg	Lys 305	Glu	Phe	Glu	Glu	Ala 310	Arg	Lys	Trp	Val	Ser 315
Lys	Lys	Leu	His	Phe 320	Glu	Lys	Asp	Val	Asp 325	Val	Asn	Leu	Phe	Glu 330
Ser	Thr	Ile	Arg	Ile 335	Leu	Gly	Gly	Leu	Leu 340	Ser	Ala	Tyr	His	Leu 345
Ser	Gly	Asp	Ser	Leu 350	Phe	Leu	Arg	Lys	Ala 355	Glu	Asp	Phe	Gly	Asn 360
Arg	Leu	Met	Pro	Ala 365	Phe	Arg	Thr	Pro	Ser 370	Lys	Ile	Pro	Tyr	Ser 375
Asp	Val	Asn	Ile	Gly 380	Thr	Gly	Val	Ala	His 385	Pro	Pro	Arg	Trp	Thr 390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe

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				410					415					420					
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys					
				425					430					435					
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe					
				440					445					450					
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr					
				455					460					465					
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu					
				470					475					480					
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg					
				485					490					495					
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val					
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Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu					
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Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly					
				530					535					540					
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr					
				545					550					555					
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu					
				560					565					570					
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val					
				575					580					585					
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr					
				590					595					600					
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys					
				605					610					615					
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe					
				620					625					630					
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln					
				635					640					645					
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe					
				650					655					660					
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp					
				665					670					675					
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala					
				680					685					690					

|||||
|||||

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
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<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
 cccccagag cgcgccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgcct ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
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 accatgtggc ttccgcact gccctgtctg tgggcggggc ccctgcact 1000
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 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

[illegible]

<220>
<221> misc feature
<222> 19-25, 65-71, 247-253, 285-291, 303-310
<223> N-myristoylation site.

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<220>  
<221> misc_feature  
<222> 27-31  
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.
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<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

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<220>
<221> misc feature
<222> 154-158
<223> N-glycosylation site.
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<220>  
<221> misc_feature  
<222> 226-233  
<223> Tyrosine kinase phosphorylation site.
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<400> 17																
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Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser		
				20					25					30		
Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser		
				35					40					45		
Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala		
				50					55					60		
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys		
				65					70					75		
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp		
				80					85					90		
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe		
				95					100					105		
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser		
				110					115					120		
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp		
				125					130					135		
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu		

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Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp	
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala	
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His	
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His	
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly	
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu	
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe	
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg	
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly	
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu	
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp	
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

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<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cttttaccta tgctgctgct 50
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gactggctcg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
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ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
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<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

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<223> Growth factor and cytokines receptors family.

<400> 22

Met	Leu	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Lys	Gly
1				5				10					15
Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser
			20					25					30
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro
			35					40					45
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Ser
			50					55					60
Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly	
				65				70					

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg cggcccgtta ggccagtgcg ccgccgctcg ccccgagggc 200
cccggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250
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tggtgtgcag cagcctggaa ctgcgcgagg tcctgcccc agatactctg 450
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gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
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<210> 24

<211> 616

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

<221> sig peptide

 $\langle 222 \rangle$ 1-33

<223> Signal peptide.

<220>

<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

<400> 24

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Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
35 40 45

Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60

Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75

Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
95 100 105

Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
110 115 120

Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
125 130 135

Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
140 145 150

Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
155 160 165

Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
170 175 180

Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
185 190 195

Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
200 205 210

Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
215 220 225

Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
230 235 240

Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
245 250 255

Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
260 265 270

Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
275 280 285

Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
290 295 300

Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
305 310 315

Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
320 325 330

Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
335 340 345

Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
350 355 360

Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
365 370 375

Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe 395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val 410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr 425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu 440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu 455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys 470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu 485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala 500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg 515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile 530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met 545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly 560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys 575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu 590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr 605	610	615

Ser

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 <213> Artificial

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 <222> 1-24

<223> Synthetic construct

<400> 25
gaggactcac caatctggtt cggc 24

<210> 26
<211> 24
<212> DNA
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<220>
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<222> 1-24
<223> Synthetic construct.

<400> 26
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<210> 27
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<222> 1-50
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<400> 27
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<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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<223> Signal peptide.

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60
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65 70 75
Lys Gly Ser Gln Lys Ser
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<211> 322
<212> PRT
<213> Homo sapiens
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<400> 31

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				20					25					30
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val
				35					40					45
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp
				50					55					60
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys
				65					70					75
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu
				80					85					90
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe
				95					100					105
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr
				110					115					120
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp
				125					130					135
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala
				140					145					150
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile
				155					160					165
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu
				170					175					180
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn
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Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr
				200					205					210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
 215 220 225
 Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
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 Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 245 250 255
 Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
 260 265 270
 Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
 275 280 285
 Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
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 Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
 305 310 315
 His Leu Val Phe Val Lys Val
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<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro	1	5	10	15
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Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val	35	40	45	
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu	50	55	60	
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu	65	70	75	
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro	80	85	90	
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys	95	100	105	
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala	110	115	120	
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg	125	130	135	
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His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu	200	205	210	
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser	215	220	225	
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Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
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Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

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Glu Pro Glu Glu Gln
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<210> 34
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<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct

<400> 34
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<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

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<210> 36
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<223> Synthetic construct.

<400> 36

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<400> 38
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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
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35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
320 325 330

Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
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<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	50		55		60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr	65		70		75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys	80		85		90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu	95		100		105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp	110		115		120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp	125		130		135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr	140		145		150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu	155		160		165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe	170		175		180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val	185		190		195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn	200		205		210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe	215		220		225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala	230		235		240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile	245		250		255
Val Glu Thr Lys Ile Cys Gln Glu	260				

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
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<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgcatgc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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aaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
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35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
170 175 180

Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
185 190 195

Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
200 205 210

Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
215 220 225

Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
230 235 240

Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
245 250 255

Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
260 265 270

Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
275 280

<210> 51
<211> 1734
<212> DNA
<213> Homo sapiens

<400> 51
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<210> 52
<211> 440
<212> PRT
<213> Homo sapiens
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<400> 52
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          20          25          30
Thr  Gly  Thr  Asn  Ile  Gly  Glu  Ala  Leu  Gly  His  Gly  Leu  Gly  Asp
          35          40          45
Ala  Leu  Ser  Glu  Gly  Val  Gly  Lys  Ala  Ile  Gly  Lys  Glu  Ala  Gly

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65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
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Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
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Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
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Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
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Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
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 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
 365 370 375
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
 380 385 390
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
 395 400 405
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
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 Ser Ser Arg Ile Pro
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<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
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Leu	Gln	Pro	Glu	Thr 785	Ser	Tyr	Asp	Ile	Lys 790	Met	Gln	Cys	Phe	Asn 795	
Glu	Gly	Gly	Glu	Ser 800	Glu	Phe	Ser	Asn	Val 805	Met	Ile	Cys	Glu	Thr 810	
Lys	Ala	Arg	Lys	Ser 815	Ser	Gly	Gln	Pro	Gly 820	Arg	Leu	Pro	Pro	Pro 825	
Thr	Leu	Ala	Pro	Pro 830	Gln	Pro	Pro	Leu	Pro 835	Glu	Thr	Ile	Glu	Arg 840	
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68

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 <222> 1-25
 <223> Synthetic construct.

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 <223> Synthetic construct.

<400> 60
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<210> 61
 <211> 42
 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 61
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<210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

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 <222> 678
 <223> unknown base

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<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

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Gln	Pro	Val	Thr	Arg 35	Ala	Glu	Thr	Thr	Pro 40	Gly	Ala	Pro	Arg	Ala 45
Leu	Ser	Thr	Leu	Gly 50	Ser	Pro	Ser	Leu	Phe 55	Thr	Thr	Pro	Gly	Val 60
Pro	Ser	Ala	Leu	Thr 65	Thr	Pro	Gly	Leu	Thr 70	Thr	Pro	Gly	Thr	Pro 75
Lys	Thr	Leu	Asp	Leu 80	Arg	Gly	Arg	Ala	Gln 85	Ala	Leu	Met	Arg	Ser 90
Phe	Pro	Leu	Val	Asp 95	Gly	His	Asn	Asp	Leu 100	Pro	Gln	Val	Leu	Arg 105
Gln	Arg	Tyr	Lys	Asn 110	Val	Leu	Gln	Asp	Val 115	Asn	Leu	Arg	Asn	Phe 120
Ser	His	Gly	Gln	Thr 125	Ser	Leu	Asp	Arg	Leu 130	Arg	Asp	Gly	Leu	Val 135
Gly	Ala	Gln	Phe	Trp 140	Ser	Ala	Ser	Val	Ser 145	Cys	Gln	Ser	Gln	Asp 150
Gln	Thr	Ala	Val	Arg 155	Leu	Ala	Leu	Glu	Gln 160	Ile	Asp	Leu	Ile	His 165
Arg	Met	Cys	Ala	Ser 170	Tyr	Ser	Glu	Leu	Glu 175	Leu	Val	Thr	Ser	Ala 180
Glu	Gly	Leu	Asn	Ser 185	Ser	Gln	Lys	Leu	Ala 190	Cys	Leu	Ile	Gly	Val 195
Xaa	Gly	Gly	His	Ser 200	Leu	Asp	Ser	Ser	Leu 205	Ser	Val	Leu	Arg	Ser 210
Phe	Tyr	Val	Leu	Gly 215	Val	Arg	Tyr	Leu	Thr 220	Leu	Thr	Phe	Thr	Cys 225
Ser	Thr	Pro	Trp	Ala 230	Glu	Ser	Ser	Thr	Lys 235	Phe	Arg	His	His	Met 240
Tyr	Thr	Asn	Val	Ser 245	Gly	Leu	Thr	Ser	Phe 250	Gly	Glu	Lys	Val	Val 255
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu	Glu Val Ser Gln Ala Pro	
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu	
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
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470	475	480
Thr Phe Thr Gln Trp Leu Cys		
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 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-25
 <223> Synthetic construct.

 <400> 64

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ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 65
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<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

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cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccacctata gaaacatcag tgggcacatt 250
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<210> 68
<211> 183
<212> PRT
<213> Homo sapiens
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   20                                25                      30

Cys  Ile  Cys  Pro  Pro  Tyr  Arg  Asn  Ile  Ser  Gly  His  Ile  Tyr  Asn
   35                                40                      45

Gln  Asn  Val  Ser  Gln  Lys  Asp  Cys  Asn  Cys  Leu  His  Val  Val  Glu
   50                                55                      60

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Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135
Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
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Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180
Met Leu Ser

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<211> 3170
<212> DNA
<213> Homo sapiens

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<211> 259
<212> PRT
<213> Homo sapiens

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Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
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Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
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Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
215 220 225

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Cys Gln Lys Ile

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<211> 1809
<212> DNA
<213> Homo sapiens

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<210> 72
<211> 363
<212> PRT
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1				5					10					15	
Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly	
				20					25					30	
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser	
				35					40					45	
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr	
				50					55					60	
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr	
				65					70					75	
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val	
				80					85					90	
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val	
				95					100					105	
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val	
				110					115					120	
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys	
				125					130					135	
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys	
				140					145					150	
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser	
				155					160					165	
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg	
				170					175					180	
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro	
				185					190					195	
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu	
				200					205					210	
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro	
				215					220					225	

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100
tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200
caccgacggc ccccgggcca ccccgcccta ctgggacggc gagaaggagg 250
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350
ctgggaccgg cagccgcccg gggccccgca cgaccgcgcg gaccgcctgc 400
tggacctcta cgcgtcgggc gagcgccgcg cctacgggcc cttttttctg 450
cgcgaccgcg tggctgtggg cgcgatgcc tttgagcgcg gtgacttctc 500
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acggtcgccc aacccacgc ggagccgccc ccccggggct ctccgggcaa 650
cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccaattcttc 750
cagcagctgg gctacgtgtt ggccacgctg ctgctcttca tcctgctact 800
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cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900
ttcgctgtgg ctgcagggga ccagatgctt tacaggagtg aggacatcca 950
gctagattac aaaaacaaca tcctgaagga gaggcgagg ctggcccaca 1000
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

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cccttccagc	ggctgggtccc	gctttcctgg	aatttggcct	gggcgtatgc	1200
agaggccgcc	tccacacccc	tccccagg	gcttgggtggc	agcatagccc	1250
ccacccctgc	ggcctttgct	cacgggtggc	cctgccacc	cctggcacia	1300
ccaaaatccc	actgatgcc	atcatgccct	cagacccttc	tgggctctgc	1350
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tggctgagga	caggggaggg	agtgaagtig	gtttgggggtg	gcctgtgttg	1900
ccactctcag	caccccat	ttgcatctgc	tggtggacct	gccaccatca	1950
caataaagtc	cccatctgat	ttttaaaaaa	aaaaaaaaaa	1989	

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
1 5 10 15

Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30

Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45

Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60

Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
110 115 120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
140 145 150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
155 160 165

Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
170 175 180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
185 190 195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
200 205 210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
215 220 225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
230 235 240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
245 250 255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
260 265 270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
275 280 285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
335 340

<210> 78
<211> 2243
<212> DNA
<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
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cactgccaag gactactgga tgttcaaact ccgcaactcc tccagcccag 300
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taccttgccg ttgcctccac cgtgccctcc atgctgtgcc tgggtggcaa 400
cttctgtctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450
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gacacttctt cctggaccgc tgggtttttt gcggtcacca ttgtctgcat 550
ggtgatcctc agcgggtgct cactgtctt cagcagcagc atctacggca 600
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gccagcctgg gcttctgtgt cactacgtc ttcttcatca ccagcctcat 1000
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 gccagtgcc aaaccagcc atgggctctt tgcaacctcc cagctgcgct 1850
 cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900
 gaaggggtct ccctggaatg gaagtcccct ggcatggtca gtcctcaggc 1950
 ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000
 ccactaacca gactggaaaa ccagaaaaga tgggccttcc atgaatgctt 2050
 cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100
 ggctggggtt ttcaaaaaaa gagggatcct catgacctgg tggcttatgg 2150
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 gccattggtt caaggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79
 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 79
 Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
 1 5 10 15
 Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
 20 25 30
 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
 35 40 45
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
 50 55 60
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
 65 70 75
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
 80 85 90
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
 95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
110 115 120

Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
125 130 135

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
140 145 150

Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
155 160 165

Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
170 175 180

Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
185 190 195

Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
200 205 210

Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
215 220 225

Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
230 235 240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
245 250 255

Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
260 265 270

Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
275 280 285

Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
290 295 300

Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
305 310 315

Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
320 325 330

Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
335 340 345

Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
350 355 360

Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
365 370 375

Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
380 385 390

Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser	
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu	
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly	
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser	
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu	Ile	
470	475	

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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gagggggcagg ggcattgtgca tgggggtggcc agcagcccct cgcattgacct 1700
ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
aaaaacacgac ccacacgagg acctgcatt aaagtatttt cggaaaaaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84
Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
1 5 10 15
Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
20 25 30
Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
35 40 45
Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
50 55 60
Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
65 70 75
Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
80 85 90
Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
95 100 105
Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
110 115 120
His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
125 130 135
Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
140 145 150
Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys		185	190	195
Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr		200	205	210
Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala		215	220	225
Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr		230	235	240
Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp		245	250	255
Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro		260	265	270
Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala		275	280	285
Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln		290	295	300
Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala		305	310	315
Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile		320	325	330
Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg		335	340	345
Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg		350	355	360
Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn		365	370	375
Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu		380	385	390
Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala		395	400	405
Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu		410	415	420
Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp		425	430	435
Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser		440	445	450
Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu				

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 tggaggaacc acgagcaggg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcgcga ggggtctgaat ttctgtctgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc cccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca tcttcttggt gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
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 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgctg 500
 tgtctgacaa tggggccctgc ttgggatata gaaaaccaa ccagccctac 550
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 ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650
 tctttgtctc gaataggcca gagtggatca tctccgaatt ggcttggttac 700
 acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750

catcg	tacat	attgt	caaca	aggct	gat	at	cgccat	ggtg	atct	gtgaca	800
cacccca	aaaa	ggcatt	ggtg	ctgat	aggg	at	gtagaga	aggctt	cacc		850
ccgagc	cctga	aggtg	atcat	ccttat	ggac	cccttt	gatg	atgac	cctgaa		900
gcaaag	aggg	gagaag	agtg	gaatt	gagat	cttat	cccta	tatgat	gctg		950
agaac	ctagg	caaag	agcac	ttcaga	aaaac	ctgtg	cctcc	tagccc	agaa		1000
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25					30

$$\frac{d^2 \phi}{dt^2} = -\frac{\partial V}{\partial \phi}$$

	320		325		330
His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys	Val		
	335		340		345
Glu His Ala Tyr	Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser	Tyr		
	350		355		360
Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val	Val		
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
	380		385		390
Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys	Gly Ile Ile Arg His	Asp		
	440		445		450
Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
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Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
	470		475		480
Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
	485		490		495
Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
	530		535		540
Phe Thr Val Asn	Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr	Asn		
	545		550		555
Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
	560		565		570
Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		
	605		610		615

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<210> 88
<211> 660
<212> PRT
<213> Homo sapiens
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				20					25					30
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu
				35					40					45
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
				50					55					60
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
				65					70					75
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
				80					85					90
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser
				95					100					105
Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu
				110					115					120
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val
				125					130					135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
140 145 150

Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
155 160 165

Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
170 175 180

Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
185 190 195

Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
200 205 210

Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
215 220 225

Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
230 235 240

Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
245 250 255

Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
260 265 270

Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
275 280 285

Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
290 295 300

Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
305 310 315

Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
320 325 330

Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
335 340 345

Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
350 355 360

Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
365 370 375

Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
380 385 390

Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
395 400 405

Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
410 415 420

Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu Glu	
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<210> 89

<211> 25

<212> DNA

<213> Artificial

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<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

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<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
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<222> 1-22
<223> Synthetic construct.

<400> 90
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<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
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<222> 1-26
<223> Synthetic construct.

<400> 92
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<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
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<222> 1-47
<223> Synthetic construct.

<400> 93
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<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

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104

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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Asn	Ala	Thr	Gly	Val 245	Ala	Met	Leu	Phe	Ser 250	Ala	Gly	Thr	Phe	Leu 255	
Tyr	Val	Ala	Thr	Val 260	His	Val	Leu	Pro	Glu 265	Val	Gly	Gly	Ile	Gly 270	
His	Ser	His	Lys	Pro 275	Asp	Ala	Thr	Gly	Gly 280	Arg	Gly	Leu	Ser	Arg 285	
Leu	Glu	Val	Ala	Ala 290	Leu	Val	Leu	Gly	Cys 295	Leu	Ile	Pro	Leu	Ile 300	
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<210> 96
<211> 25
<212> DNA
<213> Artificial
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<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.
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<400> 96
gttggtgggtg aataaaggag ggcag 25

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<210> 97
<211> 25
<212> DNA
<213> Artificial
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<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.
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<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Artificial
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<220>
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<222> 1-50
<223> Synthetic construct.
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<400> 98
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<210> 99
<211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300
ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

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gaaatgtact aaataaaaatg tacatctga 1429

$\langle 210 \rangle$ 100

<211> 401

<212> PRT

<213> Homo sapiens

$\langle 400 \rangle$ 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

cctctccctg gctgagtcct ctggcatcca tgggtgggtgg tcgagccaag 2000
aatttatggt atggagcttg tgtggcgggc ctgggtggccc tgttagctgc 2050
cgtgcgcttg tggcttggcc gctatggtaa tctcaagagc cccgagccac 2100
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<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
 20 25 30
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp	
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val	Asp His Cys Gly His Lys	
230	235	240
His Gly Pro His His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg	
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile Cys	
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe Cys	
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp	Gly Leu Val Gly Ala Ile	
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
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cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggtc 150
ttcaaggagt taaagttact tacactgtgc agtatattcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtcatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaacgtggt ccagtggtg gaccaaccac acgctggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc tttttctgt gatgggctat 600
tccatctacc gatatatcca cggtggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750
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ccttaatgat cctcagccca gcgggaacct gagggccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
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cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100
ggcagtcctg ggcccgcgaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
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 gccaacactt ccttttgcct tttgtttcct gtgcaaaca gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
 cgtgtgtgat tggttcatgc atgtaggctt cttacaatg atgggtgggcc 1650
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 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 1 5 10
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly	Lys Glu Lys His Pro	Ala Asn Leu Ile Leu Ile	170	175	180
Tyr Gly Asn Glu	Phe Asp Lys Arg Phe	Phe Val Pro Ala Glu Lys	185	190	195
Ile Val Ile Asn	Phe Ile Thr Leu Asn	Ile Ser Asp Asp Ser Lys	200	205	210
Ile Ser His Gln	Asp Met Ser Leu Leu	Gly Lys Ser Ser Asp Val	215	220	225
Ser Ser Leu Asn	Asp Pro Gln Pro Ser	Gly Asn Leu Arg Pro Pro	230	235	240
Gln Glu Glu Glu	Glu Val Lys His Leu	Gly Tyr Ala Ser His Leu	245	250	255
Met Glu Ile Phe	Cys Asp Ser Glu Glu	Asn Thr Glu Gly Thr Ser	260	265	270
Leu Thr Gln Gln	Glu Ser Leu Ser Arg	Thr Ile Pro Pro Asp Lys	275	280	285
Thr Val Ile Glu	Tyr Glu Tyr Asp Val	Arg Thr Thr Asp Ile Cys	290	295	300
Ala Gly Pro Glu	Glu Gln Glu Leu Ser	Leu Gln Glu Glu Val Ser	305	310	315
Thr Gln Gly Thr	Leu Leu Glu Ser Gln	Ala Ala Leu Ala Val Leu	320	325	330
Gly Pro Gln Thr	Leu Gln Tyr Ser Tyr	Thr Pro Gln Leu Gln Asp	335	340	345
Leu Asp Pro Leu	Ala Gln Glu His Thr	Asp Ser Glu Glu Gly Pro	350	355	360
Glu Glu Glu Pro	Ser Thr Thr Leu Val	Asp Trp Asp Pro Gln Thr	365	370	375
Gly Arg Leu Cys	Ile Pro Ser Leu Ser	Ser Phe Asp Gln Asp Ser	380	385	390
Glu Gly Cys Glu	Pro Ser Glu Gly Asp	Gly Leu Gly Glu Glu Gly	395	400	405
Leu Leu Ser Arg	Leu Tyr Glu Glu Pro	Ala Pro Asp Arg Pro Pro	410	415	420
Gly Glu Asn Glu	Thr Tyr Leu Met Gln	Phe Met Glu Glu Trp Gly	425	430	435
Leu Tyr Val Gln	Met Glu Asn		440		

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacad 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggcccagatc atcggggggc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgcg ggggtggtctc ggccgcccac tgcttcagcc 300

acagagacct ccgactggc ctggtggtgc tgggcgcca cgtcctgagt 350

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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950

gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000

tggtcagggg tgggggtggg cgggcagcgg tggggcacac ccattccaca 1050

tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
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<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
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 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
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 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acggg'gcgcca acacaggcat cggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggtctt cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
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<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
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 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
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Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	
Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly	185	190	195	
Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu	200	205	210	
Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser	215	220	225	
Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala	230	235	240	

[illegible]

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gaccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
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gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcgggggact	cggagcaggt	gcgctactgc	gcgcgcttct	cctacctctg	250
gctcaagttt	tcacttatca	tctattccac	cgtgttctgg	ctgattgggg	300
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aaaacccttg	aaagtgcctt	cctgggtcca	gccatcatcc	tcctcctcct	400
gggcgtcgtc	atgttcatgg	tctccttcat	tggtgtgctg	gcgtccctcc	450
gtgacaacct	gtaccttctc	caagcattca	tgtacatcct	tgggatctgc	500
ctcatcatgg	agctcattgg	tggcgtggtg	gccttgacct	tccggaacca	550
gaccattgac	ttcctgaacg	acaacattcg	aagaggaatt	gagaactact	600
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<210> 123
<211> 294
<212> PRT
<213> Homo sapiens
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<400> 123														
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Ser	Tyr	Leu	Trp	Leu 20	Lys	Phe	Ser	Leu	Ile 25	Ile	Tyr	Ser	Thr	Val 30
Phe	Trp	Leu	Ile	Gly 35	Ala	Leu	Val	Leu	Ser 40	Val	Gly	Ile	Tyr	Ala 45
Glu	Val	Glu	Arg	Gln 50	Lys	Tyr	Lys	Thr	Leu 55	Glu	Ser	Ala	Phe	Leu 60
Ala	Pro	Ala	Ile	Ile 65	Leu	Ile	Leu	Leu	Gly 70	Val	Val	Met	Phe	Met 75
Val	Ser	Phe	Ile	Gly 80	Val	Leu	Ala	Ser	Leu 85	Arg	Asp	Asn	Leu	Tyr 90
Leu	Leu	Gln	Ala	Phe 95	Met	Tyr	Ile	Leu	Gly 100	Ile	Cys	Leu	Ile	Met 105
Glu	Leu	Ile	Gly	Gly 110	Val	Val	Ala	Leu	Thr 115	Phe	Arg	Asn	Gln	Thr 120
Ile	Asp	Phe	Leu	Asn 125	Asp	Asn	Ile	Arg	Arg 130	Gly	Ile	Glu	Asn	Tyr 135
Tyr	Asp	Asp	Leu	Asp 140	Phe	Lys	Asn	Ile	Met 145	Asp	Phe	Val	Gln	Lys 150
Lys	Phe	Lys	Cys	Cys 155	Gly	Gly	Glu	Asp	Tyr 160	Arg	Asp	Trp	Ser	Lys 165
Asn	Gln	Tyr	His	Asp 170	Cys	Ser	Ala	Pro	Gly 175	Pro	Leu	Ala	Cys	Gly 180
Val	Pro	Tyr	Thr	Cys 185	Cys	Ile	Arg	Asn	Thr 190	Thr	Glu	Val	Val	Asn 195
Thr	Met	Cys	Gly	Tyr 200	Lys	Thr	Ile	Asp	Lys 205	Glu	Arg	Phe	Ser	Val 210
Gln	Asp	Val	Ile	Tyr 215	Val	Arg	Gly	Cys	Thr 220	Asn	Ala	Val	Ile	Ile 225
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
			245						250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
			260						265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
			275						280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
			290											

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
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<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128
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Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170 175 180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185 190 195
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200 205 210
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
470 475 480

Pro Val Ser Gln

<210> 129
<211> 2213
<212> DNA
<213> Homo sapiens

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<400> 129
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tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300
aactactact ttgttttagt tagaaciaag ctcaaaacta ctttagtta 1350
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<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
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 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
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Ser	Phe	Leu	Met	Ser											
				335											

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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cttggcgctg gcggtactgg ccccgaggc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttgagg 500
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
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attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2450
aaaaaaaaaa	aaaaaaaaaa	aaaaaa	2476		

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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens
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<400> 132
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Val  Leu  Ala  Pro  Gly  Ala  Gly  Glu  Gln  Arg  Arg  Arg  Ala  Ala  Lys
      20      25      30

Ala  Pro  Asn  Val  Val  Leu  Val  Val  Ser  Asp  Ser  Phe  Asp  Gly  Arg
      35      40      45

Leu  Thr  Phe  His  Pro  Gly  Ser  Gln  Val  Val  Lys  Leu  Pro  Phe  Ile
      50      55      60

Asn  Phe  Met  Lys  Thr  Arg  Gly  Thr  Ser  Phe  Leu  Asn  Ala  Tyr  Thr
      65      70      75

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Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
80 85 90

Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu
95 100 105

Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly
110 115 120

Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
125 130 135

His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
140 145 150

Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
155 160 165

Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
170 175 180

Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
185 190 195

Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
200 205 210

Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
215 220 225

Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
230 235 240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
245 250 255

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
260 265 270

Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
275 280 285

Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu
290 295 300

Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
305 310 315

Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
320 325 330

Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
335 340 345

Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
350 355 360

Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	
380	385	390
Asn Glu His Lys Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg	Ala Val	
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttggtgg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagaccct tctgggctcg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctctccctg 400
 gcctgcatta tctctgtggg gggcatgaga tgcacagtct tctgccagga 450

atcccgagcc	aaagacagag	tggcggtagc	aggtggagtc	tttttcatcc	500
ttggaggcct	cctgggattc	attcctgttg	cctggaatct	tcatgggatac	550
ctacgggact	tctactcacc	actggtgcct	gacagcatga	aatttgagat	600
tggagaggct	ctttacttgg	gcattatttc	ttccctgttc	tccctgatag	650
ctggaatcat	cctctgcttt	tccctgctcat	cccagagaaa	tcgctccaac	700
tactacgatg	cctaccaagc	ccaacctctt	gccacaagga	gctctccaag	750
gcctgggtcaa	cctcccaaag	tcaagagtga	gttcaattcc	tacagcctga	800
cagggtatgt	gtgaagaacc	agggggccaga	gctgggggggt	ggctgggtct	850
gtgaaaaaca	gtggacagca	ccccgagggc	cacagggtgag	ggacactacc	900
actggatcgt	gtcagaaggt	gctgctgagg	atagactgac	tttggccatt	950
ggatttgagca	aaggcagaaa	tgggggctag	tgtaacagca	tgcaggttga	1000
attgccaagg	atgctcgcca	tgccagcctt	tctgttttcc	tcaccttgct	1050
gctcccctgc	cctaagtccc	caaccctcaa	cttgaaacc	cattccctta	1100
agccaggact	cagaggatcc	ctttgccctc	tggtttacct	gggactccat	1150
ccccaacc	actaatcaca	tcccactgac	tgaccctctg	tgatcaaaga	1200
ccctctctct	ggctgagggt	ggctcttagc	tcattgctgg	ggatgggaag	1250
gagaagcagt	ggcttttgtg	ggcattgctc	taacctactt	ctcaagcttc	1300
cctccaaaga	aactgattgg	ccctggaacc	tccatcccac	tcttgttatg	1350
actccacagt	gtccagacta	atltgtgcat	gaactgaaat	aaaaccatcc	1400
tacggtatcc	agggaaacaga	aagcaggatg	caggatggga	ggacaggaag	1450
gcagcctggg	acatttaaaa	aaata			1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

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Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
20 25 30

Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
35 40 45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp	Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala	
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met	Val Thr Ser Ser Ala Ile	
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val	Val Gly Met Arg Cys Thr	
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys	Asp Arg Val Ala Val Ala	
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro	
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu	Arg Asp Phe Tyr Ser Pro	
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu	Ile Gly Glu Ala Leu Tyr	
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser	Leu Ile Ala Gly Ile Ile	
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg	Asn Arg Ser Asn Tyr Tyr	
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala	Thr Arg Ser Ser Pro Arg	
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser	Glu Phe Asn Ser Tyr Ser	
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcacgcg tcccgctggc tcagaacccat ggctgtgcca gccggcacc 150
 aggtgtggag acaagatcta caacccttg gagcagtgct gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcga atgtggtccc ccctgcacct 250
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 gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaaatt gtgaaagcag aagacgtttt ccctgagaag 400
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 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
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tgggccttga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
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acccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
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<210> 138
<211> 110
<212> PRT
<213> Homo sapiens.

<400> 138
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Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80 85 90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105
Cys Arg Ser Val Ser
110

<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

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 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
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agacttcctc	tttgtaccac	agtggctctg	gggccaggcc	tgctgcccc	1600
ctggccatcg	ccaccttccc	cagctgcctc	ctaccagcag	tttctctgaa	1650
gatctgtcaa	cagggttaagt	caatctgggg	cttccactgc	ctgcattcca	1700
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tggcctccgt	gagcaaatgg	tgtcttgggc	aatctgaggc	caggacagat	1800
gttgccccac	ccactggaga	tggtgctgag	ggaggtgggt	ggggccttct	1850
gggaaggtga	gtggagaggg	gcacctgccc	cccgccctcc	ccatccccta	1900
ctcccactgc	tcagcgcggg	ccattgcaag	ggtgccacac	aatgtcttgt	1950
ccaccctggg	acacttctga	gtatgaagcg	ggatgctatt	aaaaactaca	2000
tggggaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaga	2044

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<210> 140
<211> 311
<212> PRT
<213> Homo sapiens
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<400>	140														
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1				5					10					15	
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	

	140		145		150
Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met	Glu		
	155	160	165		
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val	Val		
	170	175	180		
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala	Ala		
	185	190	195		
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro	Leu		
	200	205	210		
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn	Arg		
	215	220	225		
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly	Ile		
	230	235	240		
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile	Pro		
	245	250	255		
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg	Gln		
	260	265	270		
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr	Pro		
	275	280	285		
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu	Asp		
	290	295	300		
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile			
	305	310			

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ctttctgccc ctcctttcct gccaccgct gcttccctggc 150
 ccttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcggcc tgaccctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tctccttgcc tgggactcgc gctgctctgg ttccccctgg 350
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc	ctgcgctgta	cctgctcaga	gggcgcccat	gtgagttggt	500
accgcctcca	ctgtccgcct	gtccactgcc	cccagcctgt	gacggagcca	550
cagcaatgct	gtcccaagtg	tgtggaacct	cacactccct	ctggactccg	600
ggccccacca	aagtcttgcc	agcacaacgg	gaccatgtac	caacacggag	650
agatcttcag	tgcccatgag	ctgttccctt	cccgcctgcc	caaccagtgt	700
gtcctctgca	gctgcacaga	gggccagatc	tactgcggcc	tcacaacctg	750
ccccgaacca	ggctgcccag	cacccctccc	actgccagac	tctgtctgcc	800
aagcctgcaa	agatgaggca	agtgagcaat	cggatgaaga	ggacagtgtg	850
cagtcgctcc	atgggggtgag	acatcctcag	gatccatggt	ccagtgatgc	900
tgggagaaa	agaggcccgg	gcaccccagc	ccccactggc	ctcagcgccc	950
ctctgagctt	catccctcgc	cacttcagac	ccaagggagc	aggcagcaca	1000
actgtcaaga	tcgtcctgaa	ggagaaacat	aagaaagcct	gtgtgcatgg	1050
cggaagacg	tactcccacg	gggaggtgtg	gcacccggcc	ttccgtgcct	1100
tcggccccctt	gccctgcac	ctatgcacct	gtgaggatgg	ccgccaggac	1150
tgccagcgtg	tgacctgtcc	caccgagtac	ccctgccgtc	accccagaaa	1200
agtggctggg	aagtgctgca	agatttgccc	agaggacaaa	gcagaccctg	1250
gccacagtga	gatcagttct	accaggtgtc	ccaaggcacc	gggccgggtc	1300
ctcgtccaca	catcggtatc	cccaagccca	gacaacctgc	gtcgttttgc	1350
cctggaacac	gaggcctcgg	acttggtgga	gatctacctc	tggaagctgg	1400
taaaagatga	ggaaactgag	gctcagagag	gtgaagtacc	tggcccaagg	1450
ccacacagcc	agaatcttcc	acttgactca	gatcaagaaa	gtcaggaagc	1500
aagacttcca	gaaagaggca	cagcacttcc	gactgctcgc	tggcccccac	1550
gaaggctcact	ggaacgtctt	cctagcccag	accctggagc	tgaaggtcac	1600
ggccagtcca	gacaaaagtga	ccaagacata	acaaaagacct	aacagttgca	1650
gatatgagct	gtataattgt	tgttattata	tattaataaaa	taagaagttg	1700
cattaccctc	aaaaaaaaaa	aaaaaaaaaa	aa	1732	

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<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142
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Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
1 5 10 15

Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
20 25 30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
35 40 45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
50 55 60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
65 70 75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
80 85 90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
95 100 105

Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
110 115 120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
125 130 135

Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
140 145 150

Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
155 160 165

Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
170 175 180

Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
185 190 195

His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
200 205 210

Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
215 220 225

Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
230 235 240

Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
245 250 255

Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
260 265 270

Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
275 280 285

Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

ccagcggaga gtccggaccg agataccatg ccaggactct ccgggggtcct 500
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgcca tggggccag caccctctc ctcatottgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagaccacaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
 gcaaacagag aagatctacg tgtttagatgg gacacagaat gacacagcct 650
 ttgtcttccc aaggtgcgt gacttcaccc ttgccatggc tgcccggaaa 700
 gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
 aaccgaacag tggtaggacag ctcaagtatc ccagcagagg ggctgatccc 900
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
 tctatgtcgt ctataacacc cgtcctgcca gtcgggcccg catccagtgc 1150
 tcctttgatg ccagcggcac cctgaccct gaacgggcag cactccctta 1200
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
 catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
 ttcctcattc ttcaaagtgt gccagttgt ggctcaaac ctctatatatt 1450
 ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
 ttcctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
 cccagacca gggctctaac cttgtatgcg ggcaggcca gggagcaggc 1650
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 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 146
 Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
 1 5 10 15
 Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
 20 25 30
 Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
 35 40 45
 Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
 50 55 60
 Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
 65 70 75
 Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
 80 85 90
 Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
 95 100 105
 Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
 110 115 120
 Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
 125 130 135
 Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
 140 145 150
 Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
 155 160 165
 Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
 170 175 180
 Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
 185 190 195
 Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
 200 205 210
 Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
 215 220 225
 Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
 230 235 240
 Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
 245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala	260	265	270
Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala	275	280	285
Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys	290	295	300
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro	305	310	315
Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr	320	325	330
Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile	335	340	345
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala	350	355	360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu	365	370	375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly	380	385	390
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu	395	400	405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttgggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacaggagcg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggaggggagc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtaacagat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950
 ttctttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
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 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
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 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc cttcctcccc aggggtgaaa ttaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctc ctcccagatc caaagtcccc 1750
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgtga tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

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<210> 148
<211> 500
<212> PRT
<213> Homo sapiens
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<400>	148													
Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly
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Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
				20					25					30
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggccttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtgccggc ggggccgcgg ggcaggtgga 250
cgcgtgcgcg ggccccgggt tgcggggcga gccagccac cccttcctta 300
gggacgagcc tcccacggcc caggccccga ggaccgggc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt	tgggcgactg	ctggaccctc	ttccaccacc	tttcaggcgc	450
cgctcggccc	ctcgccgacc	acccctccgg	cggcggaacg	cacttcgacc	500
acctctcagg	cgccgaccag	acccgcgcgc	accacccttt	cga cgaccac	550
tggcccggcg	ccgaccaccc	ctgtagcgac	caccgtaccg	gcgcccacga	600
ctccccggac	cccgaccccc	gatctcccca	gcagcagcaa	cagcagcgtc	650
ctccccaccc	cacctgccac	cgaggccccc	tcttcgcctc	ctccagagta	700
tgatatgtaac	tgctctgtgg	ttggaagcct	gaatgtgaat	cgctgcaacc	750
agaccacagg	gcagtgtgag	tgtcggccag	gttatcaggg	gcttcactgt	800
gaaacctgca	aagagggctt	ttacctaaat	tacacttctg	ggctctgtca	850
gccatgtgac	tgtagtccac	atggagctct	cagcataccg	tgcaacaggt	900
aagcaacaga	gggtggaact	gaagttttatt	ttattttagc	aagggaaaaa	950
aaaaggctgc	tactctcaag	gaccatactg	gtttaaacaa	aggaggatga	1000
gggtcataga	tttacaaaat	attttatata	cttttattct	cttactttat	1050
atgttatatt	taatgtcagg	atttaaaaac	atctaattta	ctgatttagt	1100
tcttcaaaag	cactagagtc	gccaatTTTT	ctctgggata	atctctgtaa	1150
atctcatggg	aaaaaattat	tgaagaataa	atctgctttc	tggaagggct	1200
ttcaggcatg	aaacctgcta	ggagggttag	aatgtttctt	atgtttatta	1250
atataccatt	ggagtttgag	gaaatttggt	gtttggttta	tttttctctc	1300
taatcaaaat	tctacatttg	tttctttgga	catctaaagc	ttaacctggg	1350
ggtaccctaa	tttatttaac	tagtggttaag	tagactgggt	ttactctatt	1400
taccagtaca	tttttgagac	caaaagtaga	ttaagcagga	attatcttta	1450
aactattatg	ttatttgagg	gtaatttaat	ctagtggaat	aatgtactgt	1500
tatctaagca	tttgcccttg	actgcactga	aagtaattat	tctttgacct	1550
tatgtgaggc	acttggcttt	ttgtggaccc	caagtcaaaa	aactgaagag	1600
acagtattaa	ataatgaaaa	aaataatgac	aggttatact	cagtgttaacc	1650
tgggtataac	ccaagatctg	ctgccactta	cgagctgtgt	tccttgggca	1700
agtaatttcc	tttactgag	cttgtttctt	ctcaagggtg	ttgtgaagat	1750
taaatgagtt	gatatatata	aaatgcctag	cacatgtcac	tcaataaatt	1800
ctggtttgtt	ttaatttcaa	aggaatatta	tggactgaaa	tgagagaaca	1850


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<210> 157
<211> 689
<212> DNA
<213> Homo sapiens
```

```

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggcctt ggtctcgggtg cccagggccc aggccgtgtg gttgggaaga 100
ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
ccgggaaaag ggctttgcc a tggagaagga catgaagaac gtcgtggggg 200
tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
tgctggccac caacttcaga gactatgcc a tcatcttcac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
gggtcctgtg acctcgcca gtgtccaccc acctcgctca gcggctcccg 650
gggcccagca ccagctcaga ataaagcgat tccacaqca 689

```

```
<210> 158
<211> 163
<212> PRT
<213> Homo sapiens
```

```

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1          5          10          15

Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20          25          30

Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35          40          45

Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50          55          60

Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65          70          75

His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80          85          90

```


Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacggt cctcgcggc cctggcacct ctaaccccag acatgctgct 50
 gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100
 gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150
 gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacct 200
 tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctct 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
 ccctggacc cctccaccac ccgctcctcg gtgtcacc tcacccaca 650
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtactccc agaggggcag tctctgcgcc 850
 tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

ggtgctggag	ctgccttggg	tgacacctgag	ggatgcagct	gaattcacct	1000
gcagagctca	gaaccctctc	ggctctcagc	aggtctacct	gaacgtctcc	1050
ctgcagagca	aagccacatc	aggagtgact	caggggggtg	tcgggggagc	1100
tggagccaca	gccctgggtct	tcctgtcctt	ctgcgtcatc	ttcgtttgtag	1150
tgaggctcctg	caggaagaaa	tcggcaaggc	cagcagcggg	cgtgggagat	1200
acgggcatag	aggatgcaaa	cgctgtcagg	ggttcagcct	ctcagggggc	1250
cctgactgaa	ccttgggcag	aagacagtcc	cccagaccag	cctccccag	1300
cttctgccccg	ctcctcagtg	ggggaaggag	agctccagta	tgcattccctc	1350
agcttccaga	tggatgaagcc	ttgggactcg	cggggacagg	aggccactga	1400
caccgagtag	tcggagatca	agatccacag	atgagaaact	gcagagactc	1450
accctgattg	agggatcaca	gccctccag	gcaagggaga	agtcagaggc	1500
tgattcttgt	agaattaaca	gccctcaacg	tgatgagcta	tgataaact	1550
atgaattatg	tgagagtgga	aaagcacaca	ggcttttagag	tcaaagtatc	1600
tcaaacctga	atccacactg	tgccctccct	tttatTTTTT	taactaaaag	1650
acagacaaat	tccta				1665

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<210> 160
<211> 463
<212> PRT
<213> Homo sapiens
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<400>	160													
Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
125	130	135	
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu	Pro	Trp	Ala	Glu 410	Asp	Ser	Pro	Pro	Asp 415	Gln	Pro	Pro	Pro	Ala 420
Ser	Ala	Arg	Ser	Ser 425	Val	Gly	Glu	Gly	Glu 430	Leu	Gln	Tyr	Ala	Ser 435
Leu	Ser	Phe	Gln	Met 440	Val	Lys	Pro	Trp	Asp 445	Ser	Arg	Gly	Gln	Glu 450
Ala	Thr	Asp	Thr	Glu 455	Tyr	Ser	Glu	Ile	Lys 460	Ile	His	Arg		

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<210> 161
<211> 739
<212> DNA
<213> Homo sapiens
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<400> 161
gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400
tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
gctcccacc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739
```

```
<210> 162
<211> 170
<212> PRT
<213> Homo sapiens
```

168

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

```
<210> 165
<211> 21
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.
```

```
<400> 165
gtcctccgga aagtccttat c 21
```

```
<210> 166
<211> 25
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.
```

```
<400> 166
gcctagtgtt cgggaacgca qcttc 25
```

```
<210> 167
<211> 50
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.
```

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggaq 50

```
<210> 168
<211> 45
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.
```

```
<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45
```

```
<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens
```

<400> 169

gttcgcgacaga	tgcagagagtt	gaggtggtctg	cgggactgga	agtcacgcggg	50
cagaggtctc	acagcagcca	aggaacctgg	ggcccgtcc	tccccctcc	100
aggccatgag	gattctgcag	ttaatcctgc	ttgctctggc	aacagggtctt	150
gtaggggggag	agaccaggat	catcaagggg	ttcgagtgca	agcctcactc	200
ccagccctgg	caggcagccc	tgttcgagaa	gacgcggcta	ctctgtgggg	250
cgacgctcat	cgccccacga	tggctcctga	cagcagccca	ctgcctcaag	300
ccccgctaca	tagttcacct	ggggcagcac	aacctccaga	aggaggaggg	350
ctgtgagcag	acccggacag	ccactgagtc	cttccccac	cccggcttca	400
acaacagcct	ccccaaacaa	gaccaccgca	atgacatcat	gctggtgaag	450
atggcatcgc	cagtctccat	cacctgggct	gtgcgacccc	tcacctctc	500
ctcacgctgt	gtcactgctg	gcaccagctg	cctcatttcc	ggctggggca	550
gcacgtccag	ccccagtta	cgcttgctc	acaccttgcg	atgcgccaac	600
atcaccatca	ttgagcacca	gaagtgtgag	aacgcctacc	ccggcaacat	650
cacagacacc	atggtgtgtg	ccagcgtgca	ggaagggggc	aaggactcct	700
gccaggtga	ctccgggggc	cctctggtct	gtaaccagtc	tcttcaaggc	750
attatctcct	ggggccagga	tccgtgtgcg	atcacccgaa	agcctggtgt	800
ctacacgaaa	gtctgcaa	atgtggactg	gatccaggag	acgatgaaga	850
acaattagac	tggaccacc	caccacagcc	catcacctc	catttccact	900
tggtgtttgg	ttcctgttca	ctctgtta	aagaaaccct	aagccaagac	950
cctctacgaa	cattctttgg	gcctcctgga	ctacaggaga	tgctgtcact	1000
taataatcaa	cctgggggtc	gaaatcagtg	agacctggat	tcaattctg	1050
ccttgaaata	ttgtgactct	gggaatgaca	acacctggtt	tgttctctgt	1100
tgtaacccca	gccccaaaga	cagctcctgg	ccatataatca	aggtttcaat	1150
aaatatttgc	taaatgaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaa	1204				

```
<210> 170
<211> 250
<212> PRT
<213> Homo sapiens
```

```
<400> 170
Met  Arg  Ile  Leu  Gln  Leu  Ile  Leu  Leu  Ala  Leu  Ala  Thr  Gly  Leu
  1             5             10             15
```

Val	Gly	Gly	Glu	Thr 20	Arg	Ile	Ile	Lys	Gly 25	Phe	Glu	Cys	Lys	Pro 30
His	Ser	Gln	Pro	Trp 35	Gln	Ala	Ala	Leu	Phe 40	Glu	Lys	Thr	Arg	Leu 45
Leu	Cys	Gly	Ala	Thr 50	Leu	Ile	Ala	Pro	Arg 55	Trp	Leu	Leu	Thr	Ala 60
Ala	His	Cys	Leu	Lys 65	Pro	Arg	Tyr	Ile	Val 70	His	Leu	Gly	Gln	His 75
Asn	Leu	Gln	Lys	Glu 80	Glu	Gly	Cys	Glu	Gln 85	Thr	Arg	Thr	Ala	Thr 90
Glu	Ser	Phe	Pro	His 95	Pro	Gly	Phe	Asn	Asn 100	Ser	Leu	Pro	Asn	Lys 105
Asp	His	Arg	Asn	Asp 110	Ile	Met	Leu	Val	Lys 115	Met	Ala	Ser	Pro	Val 120
Ser	Ile	Thr	Trp	Ala 125	Val	Arg	Pro	Leu	Thr 130	Leu	Ser	Ser	Arg	Cys 135
Val	Thr	Ala	Gly	Thr 140	Ser	Cys	Leu	Ile	Ser 145	Gly	Trp	Gly	Ser	Thr 150
Ser	Ser	Pro	Gln	Leu 155	Arg	Leu	Pro	His	Thr 160	Leu	Arg	Cys	Ala	Asn 165
Ile	Thr	Ile	Ile	Glu 170	His	Gln	Lys	Cys	Glu 175	Asn	Ala	Tyr	Pro	Gly 180
Asn	Ile	Thr	Asp	Thr 185	Met	Val	Cys	Ala	Ser 190	Val	Gln	Glu	Gly	Gly 195
Lys	Asp	Ser	Cys	Gln 200	Gly	Asp	Ser	Gly	Gly 205	Pro	Leu	Val	Cys	Asn 210
Gln	Ser	Leu	Gln	Gly 215	Ile	Ile	Ser	Trp	Gly 220	Gln	Asp	Pro	Cys	Ala 225
Ile	Thr	Arg	Lys	Pro 230	Gly	Val	Tyr	Thr	Lys 235	Val	Cys	Lys	Tyr	Val 240
Asp	Trp	Ile	Gln	Glu 245	Thr	Met	Lys	Asn	Asn 250					

<210> 171

<211> 25

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.


```
<400> 171
  ggctgcgggg ctggaagtca tcggg 25
```

```
<210> 172
<211> 24
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
```

```
<400> 172
ctccaggcca tgaggattct gcag 24
```

```
<210> 173
<211> 18
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.
```

<400> 173
cctctggtct gtaaccag 18

```
<210> 174
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 174
tctgtgatgt tgccggggta ggcg 24
```

```
<210> 175
<211> 25
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.
```

```
<400> 175
  cgtgtagaca ccaggctttc gggtg 25
```

<210>	176
<211>	18
<212>	DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttgggtgtg ggcaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca ttgcatatg gaaaggaagg ctatgcagaa 400

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15
Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
20 25 30
Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
35 40 45
Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
50 55 60
Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
65 70 75
Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
80 85 90
Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
95 100 105
Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
110 115 120
Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
125 130 135
Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
140 145 150

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 184
 gatgtctgcc accccaag 18

<210> 185
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 185
 gcatcctgat atgacttgct acgtggc 27

<210> 186
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 186
 tacaagaggg aagaggagtt gcac 24

<210> 187
 <211> 52
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

<400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
 cc 52

<210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 188
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
 ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcc 100

cccaaagtgt tctgtgtgca ataacaactca ctgcacctgc aacctatggat 150
 atactttctgg atctggggcag aaactatttca cattcccctt ggagacatgt 200
 aacgccaggc atgggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcaactga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

```

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atgggggtca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cactctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgtctcag 600
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtg agggggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggccccc tgggtgtgtg gggagtcctt 750
caaggtctgg tgcctgggg gtctgtgggg ccctgtggac aagatggcat 800

```

```
ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
tcatgaggaa caactgacct gtttcctcca cctccacccc caccaccttaa 900
cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
gccagccctt ctaagacca cgagcggggt gagagaagtg tgcaatagtc 1050
tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091
```

<213> Homo sapiens

Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
1 5 10 15

Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
20 25 30

Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
35 40 45

Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
50 55 60

Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
65 70 75

Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
80 85 90

Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
95 100 105

Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
110 115 120

Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
125 130 135

Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
140 145 150

Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
155 160 165

Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
170 175 180

Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
185 190 195

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

				200						205					210
Gln	Gly	Leu	Val	Ser 215	Trp	Gly	Ser	Val	Gly 220	Pro	Cys	Gly	Gln	Asp 225	
Gly	Ile	Pro	Gly	Val 230	Tyr	Thr	Tyr	Ile	Cys 235	Lys	Tyr	Val	Asp	Trp 240	
Ile	Arg	Met	Ile	Met 245	Arg	Asn	Asn								

```
<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens
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<400>	195				
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tcgccatgtc	gggcgagctc	agcaacaggt	tccaaggagg	gaaggcggtc	150
ggcttgctca	aagcccggca	ggagaggagg	ctggccgaga	tcaaccggga	200
gtttctgtgt	gaccagaagt	acagtgatga	agagaacctt	ccagaaaagc	250
tcacagcctt	caaagagaag	tacatggagt	ttgacctgaa	caatgaaggc	300
gagattgacc	tgatgtcttt	aaagaggatg	atggagaagc	ttggtgtccc	350
caagaccac	ctggagatga	agaagatgat	ctcagaggtg	acaggagggg	400
tcagtgcac	tatatcctac	cgagactttg	tgaacatgat	gctggggaaa	450
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tgccctgagg	accccgctg	gactccccag	ccttcccacc	ccatacctcc	600
ctcccgatct	tgctgccctt	cttgacacac	tgtgatctct	ctctctctca	650
tttgtttggt	cattgagggg	ttgtttgtgt	tttcatcaat	gtctttgtaa	700
agcacaaatt	atctgcctta	aaggggctct	gggtcgggga	atcctgagcc	750
ttgggtcccc	tcctctcttt	cttccctcct	tccccgctcc	ctgtgcagaa	800
gggctgatat	caaacaaaa	actagagggg	gcagggccag	ggcagggagg	850
cttccagcct	gtgttcccct	cacttgaggg	aaccagcact	ctccatcctt	900
tcagaaagtc	tccaagccaa	gttcaggctc	actgacctgg	ctctgacgag	950
gaccccaggc	cactctgaga	agaccttgga	gtagggacaa	ggctgcaggg	1000
cctctttcgg	gtttccttgg	acagtgccat	ggttccagtg	ctctgggtgtc	1050

acccaggaca cagccactcg gggcccccgt gccccagctg atccccactc 1100
 attccacacc tcttctcatc ctcaagtgtg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

[illegible]

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tgacagccac	aaggatgggt	tcagctgctc	ctgccctctg	ggctttgagg	3050
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gcctaactac	acaggtgagc	tatgcgacga	ggtgattgac	cactgtgtgc	3200
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ggattcagct	gcgagtgtgt	ccctggctac	agcgggaagc	tctgtgagac	3300
agacaatgat	gactgtgtgg	cccacaagt	ccgccacggg	gccagtgcg	3350
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tccaaccaca	gtgtacagt	tggagacagt	gaatgatggg	cagtttcaca	3800
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acagtccttg	ggggtgtcac	caggctgcaa	gtcctgcacc	gtgtgcaagc	4100
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cggccacaga	tgccaccatg	gaaaatgtgt	ggcaactggg	acctcataca	4250
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gactctgcc	atgcctgctc	agccttcaag	tgtcaccatg	ggcagtgcca	4350

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ctaagcccct gccgcctgc ctgccacctc tcggactcca gcttgatgga 4700
gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750
agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
1 5 10 15
Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
20 25 30
Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser	
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe	
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg	
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg	
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn	
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys	
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys	
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu	
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val	
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn	
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser	
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr	
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu	
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly	
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys	
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala	
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln	
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val	
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met	
740	745	750

Pro	Lys	Asp	Val	Thr 755	Glu	Leu	Tyr	Leu	Glu 760	Gly	Asn	His	Leu	Thr 765
Ala	Val	Pro	Arg	Glu 770	Leu	Ser	Ala	Leu	Arg 775	His	Leu	Thr	Leu	Ile 780
Asp	Leu	Ser	Asn	Asn 785	Ser	Ile	Ser	Met	Leu 790	Thr	Asn	Tyr	Thr	Phe 795
Ser	Asn	Met	Ser	His 800	Leu	Ser	Thr	Leu	Ile 805	Leu	Ser	Tyr	Asn	Arg 810
Leu	Arg	Cys	Ile	Pro 815	Val	His	Ala	Phe	Asn 820	Gly	Leu	Arg	Ser	Leu 825
Arg	Val	Leu	Thr	Leu 830	His	Gly	Asn	Asp	Ile 835	Ser	Ser	Val	Pro	Glu 840
Gly	Ser	Phe	Asn	Asp 845	Leu	Thr	Ser	Leu	Ser 850	His	Leu	Ala	Leu	Gly 855
Thr	Asn	Pro	Leu	His 860	Cys	Asp	Cys	Ser	Leu 865	Arg	Trp	Leu	Ser	Glu 870
Trp	Val	Lys	Ala	Gly 875	Tyr	Lys	Glu	Pro	Gly 880	Ile	Ala	Arg	Cys	Ser 885
Ser	Pro	Glu	Pro	Met 890	Ala	Asp	Arg	Leu	Leu 895	Leu	Thr	Thr	Pro	Thr 900
His	Arg	Phe	Gln	Cys 905	Lys	Gly	Pro	Val	Asp 910	Ile	Asn	Ile	Val	Ala 915
Lys	Cys	Asn	Ala	Cys 920	Leu	Ser	Ser	Pro	Cys 925	Lys	Asn	Asn	Gly	Thr 930
Cys	Thr	Gln	Asp	Pro 935	Val	Glu	Leu	Tyr	Arg 940	Cys	Ala	Cys	Pro	Tyr 945
Ser	Tyr	Lys	Gly	Lys 950	Asp	Cys	Thr	Val	Pro 955	Ile	Asn	Thr	Cys	Ile 960
Gln	Asn	Pro	Cys	Gln 965	His	Gly	Gly	Thr	Cys 970	His	Leu	Ser	Asp	Ser 975
His	Lys	Asp	Gly	Phe 980	Ser	Cys	Ser	Cys	Pro 985	Leu	Gly	Phe	Glu	Gly 990
Gln	Arg	Cys	Glu	Ile 995	Asn	Pro	Asp	Asp	Cys 1000	Glu	Asp	Asn	Asp	Cys 1005
Glu	Asn	Asn	Ala	Thr 1010	Cys	Val	Asp	Gly	Ile 1015	Asn	Asn	Tyr	Val	Cys 1020
Ile	Cys	Pro	Pro	Asn 1025	Tyr	Thr	Gly	Glu	Leu 1030	Cys	Asp	Glu	Val	Ile 1035
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys

Cys Ile Pro Leu Asp	Lys Gly Phe Ser Cys	Glu Cys Val Pro Gly
1055	1060	1065
Tyr Ser Gly Lys Leu Cys	Glu Thr Asp Asn Asp	Asp Cys Val Ala
1070	1075	1080
His Lys Cys Arg His	Gly Ala Gln Cys Val	Asp Thr Ile Asn Gly
1085	1090	1095
Tyr Thr Cys Thr Cys	Pro Gln Gly Phe Ser	Gly Pro Phe Cys Glu
1100	1105	1110
His Pro Pro Pro Met	Val Leu Leu Gln Thr	Ser Pro Cys Asp Gln
1115	1120	1125
Tyr Glu Cys Gln Asn	Gly Ala Gln Cys Ile	Val Val Gln Gln Glu
1130	1135	1140
Pro Thr Cys Arg Cys	Pro Pro Gly Phe Ala	Gly Pro Arg Cys Glu
1145	1150	1155
Lys Leu Ile Thr Val	Asn Phe Val Gly Lys	Asp Ser Tyr Val Glu
1160	1165	1170
Leu Ala Ser Ala Lys	Val Arg Pro Gln Ala	Asn Ile Ser Leu Gln
1175	1180	1185
Val Ala Thr Asp Lys	Asp Asn Gly Ile Leu	Leu Tyr Lys Gly Asp
1190	1195	1200
Asn Asp Pro Leu Ala	Leu Glu Leu Tyr Gln	Gly His Val Arg Leu
1205	1210	1215
Val Tyr Asp Ser Leu	Ser Ser Pro Pro Thr	Thr Val Tyr Ser Val
1220	1225	1230
Glu Thr Val Asn Asp	Gly Gln Phe His Ser	Val Glu Leu Val Thr
1235	1240	1245
Leu Asn Gln Thr Leu	Asn Leu Val Val Asp	Lys Gly Thr Pro Lys
1250	1255	1260
Ser Leu Gly Lys Leu	Gln Lys Gln Pro Ala	Val Gly Ile Asn Ser
1265	1270	1275
Pro Leu Tyr Leu Gly	Gly Ile Pro Thr Ser	Thr Gly Leu Ser Ala
1280	1285	1290
Leu Arg Gln Gly Thr	Asp Arg Pro Leu Gly	Gly Phe His Gly Cys
1295	1300	1305
Ile His Glu Val Arg	Ile Asn Asn Glu Leu	Gln Asp Phe Lys Ala
1310	1315	1320
Leu Pro Pro Gln Ser	Leu Gly Val Ser Pro	Gly Cys Lys Ser Cys
1325	1330	1335

Thr	Val	Cys	Lys	His 1340	Gly	Leu	Cys	Arg	Ser 1345	Val	Glu	Lys	Asp	Ser 1350
Val	Val	Cys	Glu	Cys 1355	Arg	Pro	Gly	Trp	Thr 1360	Gly	Pro	Leu	Cys	Asp 1365
Gln	Glu	Ala	Arg	Asp 1370	Pro	Cys	Leu	Gly	His 1375	Arg	Cys	His	His	Gly 1380
Lys	Cys	Val	Ala	Thr 1385	Gly	Thr	Ser	Tyr	Met 1390	Cys	Lys	Cys	Ala	Glu 1395
Gly	Tyr	Gly	Gly	Asp 1400	Leu	Cys	Asp	Asn	Lys 1405	Asn	Asp	Ser	Ala	Asn 1410
Ala	Cys	Ser	Ala	Phe 1415	Lys	Cys	His	His	Gly 1420	Gln	Cys	His	Ile	Ser 1425
Asp	Gln	Gly	Glu	Pro 1430	Tyr	Cys	Leu	Cys	Gln 1435	Pro	Gly	Phe	Ser	Gly 1440
Glu	His	Cys	Gln	Gln 1445	Glu	Asn	Pro	Cys	Leu 1450	Gly	Gln	Val	Val	Arg 1455
Glu	Val	Ile	Arg	Arg 1460	Gln	Lys	Gly	Tyr	Ala 1465	Ser	Cys	Ala	Thr	Ala 1470
Ser	Lys	Val	Pro	Ile 1475	Met	Glu	Cys	Arg	Gly 1480	Gly	Cys	Gly	Pro	Gln 1485
Cys	Cys	Gln	Pro	Thr 1490	Arg	Ser	Lys	Arg	Arg 1495	Lys	Tyr	Val	Phe	Gln 1500
Cys	Thr	Asp	Gly	Ser 1505	Ser	Phe	Val	Glu	Glu 1510	Val	Glu	Arg	His	Leu 1515
Glu	Cys	Gly	Cys	Leu 1520	Ala	Cys	Ser							

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<210> 199
<211> 24
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
```

```
<400> 199
atggagattc ctgccaaactt gccg 24
```

```
<210> 200
<211> 24
<212> DNA
<213> Artificial
```

<220>

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattht gcatcccact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcattgtgt aaaaacgcc aactgaatat atcatgcccc 100
tattaaaact tgtacatggc tcccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctcagttggt 450
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
ccctagtaca gctgctgga agattgacat cccaagattg ggagaggggt 600
catctgatcg tggcaggtgg ttatgacgag agagtccctg agaatgtgga 650
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950
accttcctta aaagccacca tgggcctggc tgggaagagcc agagtgaagg 1000
aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050
aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100
ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150
atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250
tttatgctat aatcattcca aattttgcca gtgttaagtt acaaatgtgg 1300
tgtcattcca tgttcagcag agtattttta ttatattttc tcgggattat 1350
tgctcttctg totataaatt ttgaatgata ctgtgcctta attggttttc 1400
atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
tcaactgcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550
catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
actgagatat aataaaagggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
 275 280 285
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
 290 295 300
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
 305 310 315
 Arg Tyr Val Thr Lys Leu Leu Val
 320

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgata ttgcgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100
 tctaccteta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
 tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250
 ccttctgggt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg ctccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct	cagatattgt	cagcatgtgc	tttgtgaaac	tgttcgaact	1050
gccaaactga	ctccagtttc	tgcccagctt	caagatattg	aaggaaaaat	1100
tgaccgattt	attattccta	gagagaccct	cgtcctttat	gcccttggtg	1150
tggtacttca	ggatccta	acttggccat	ctccacacaa	gtttgatcca	1200
gatcggtttg	atgatgaatt	agtaatgaaa	actttttcct	cacttggatt	1250
ctcaggcaca	caggagtgtc	cagagttgag	gtttgcatat	atgggtgacca	1300
cagtacttct	tagtgtattg	gtgaagagac	tgcacctact	ttctgtggag	1350
ggacagggtta	ttgaaacaaa	gtatgaactg	gtaacatcat	caagggaaga	1400
agcttggatc	actgtctcaa	agagatat	aaattttata	catttaaaat	1450
cattgttaaa	ttgattgagg	aaaacaacca	tttaaaaaaa	atctatgttg	1500
aatcctttta	taaaccagta	tcactttgta	atataaacac	ctatttgtac	1550
ttaa	1554				

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<210> 212
<211> 462
<212> PRT
<213> Homo sapiens
```

```

<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
  1          5          10          15
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
          20          25          30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
          35          40          45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
          50          55          60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
          65          70          75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
          80          85          90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
          95          100          105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
          110          115          120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
          125          130          135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

```

Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	1	5	10	15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	20	25	30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	35	40	45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	50	55	60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	65	70	75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	80	85	90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	95	100	105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	110	115	120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	125	130	135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	140	145	150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	155	160	165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	170	175	180	
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<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcgaa 200

gcggggccac atctcaccta agtccccgcc catggccaat tccactctcc 250
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<210> 218
<211> 252
<212> PRT
<213> Homo sapiens
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<400> 218														
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Glu	Asp	Pro	Glu	Arg 35	Asp	Asp	His	Glu	Gly 40	Gln	Pro	Arg	Pro	Arg 45
Val	Pro	Arg	Lys	Arg 50	Gly	His	Ile	Ser	Pro 55	Lys	Ser	Arg	Pro	Met 60
Ala	Asn	Ser	Thr	Leu 65	Leu	Gly	Leu	Leu	Ala 70	Pro	Pro	Gly	Glu	Ala 75
Trp	Gly	Ile	Leu	Gly 80	Gln	Pro	Pro	Asn	Arg 85	Pro	Asn	His	Ser	Pro 90
Pro	Pro	Ser	Ala	Lys 95	Val	Lys	Lys	Ile	Phe 100	Gly	Trp	Gly	Asp	Phe 105
Tyr	Ser	Asn	Ile	Lys 110	Thr	Val	Ala	Leu	Asn 115	Leu	Leu	Val	Thr	Gly 120
Lys	Ile	Val	Asp	His 125	Gly	Asn	Gly	Thr	Phe 130	Ser	Val	His	Phe	Gln 135
His	Asn	Ala	Thr	Gly 140	Gln	Gly	Asn	Ile	Ser 145	Ile	Ser	Leu	Val	Pro 150
Pro	Ser	Lys	Ala	Val 155	Glu	Phe	His	Gln	Glu 160	Gln	Gln	Ile	Phe	Ile 165
Glu	Ala	Lys	Ala	Ser 170	Lys	Ile	Phe	Asn	Cys 175	Arg	Met	Glu	Trp	Glu 180
Lys	Val	Glu	Arg	Gly 185	Arg	Arg	Thr	Ser	Leu 190	Cys	Thr	His	Asp	Pro 195
Ala	Lys	Ile	Cys	Ser 200	Arg	Asp	His	Ala	Gln 205	Ser	Ser	Ala	Thr	Trp 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
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Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
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Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
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<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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ttcaaataat ccataatctaa atttagtgca atatctgtc ttttgtatag 2000
gtcatatgaa ttcataaaat ttttatgtc tgttatagaa taaagattaa 2050
tatatgttaa aaaaa 2065

<210> 220
<211> 201
<212> PRT
<213> Homo sapiens

<400> 220
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20 25 30
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
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<212> DNA
<213> Artificial

<220>
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

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Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
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Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
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Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
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Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
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Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
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His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
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Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
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Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
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Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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Ser Arg

<210> 226

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<210> 227
<211> 832
<212> PRT
<213> Homo sapiens
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Val  Glu  Ser  His  Leu  Gly  Val  Leu  Gly  Pro  Lys  Asn  Val  Ser  Gln
                   20             25             30

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 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
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 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
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 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
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 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
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 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
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 245 250 255
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
 260 265 270
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
 275 280 285
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 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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Asp	Ser	Phe	Pro	Gly 350	Ser	Ser	Pro	Tyr	Glu 355	Gly	Tyr	Asn	Tyr	Gly 360
Ser	Phe	Glu	Asn	Val 365	Ser	Gly	Ser	Thr	Asp 370	Gly	Leu	Val	Asp	Ser 375
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Glu	Pro	Val	Gly	Thr 395	Arg	Pro	Arg	Val	Asp 400	Ser	Met	Ser	Ser	Val 405
Glu	Glu	Asp	Asp	Tyr 410	Asp	Thr	Leu	Thr	Asp 415	Ile	Asp	Ser	Asp	Lys 420
Asn	Val	Ile	Arg	Thr 425	Lys	Gln	Tyr	Leu	Tyr 430	Val	Ala	Asp	Leu	Ala 435
Arg	Lys	Asp	Lys	Arg 440	Val	Leu	Arg	Lys	Lys 445	Tyr	Gln	Ile	Tyr	Phe 450
Trp	Asn	Ile	Ala	Thr 455	Ile	Ala	Val	Phe	Tyr 460	Ala	Leu	Pro	Val	Val 465
Gln	Leu	Val	Ile	Thr 470	Tyr	Gln	Thr	Val	Val 475	Asn	Val	Thr	Gly	Asn 480
Gln	Asp	Ile	Cys	Tyr 485	Tyr	Asn	Phe	Leu	Cys 490	Ala	His	Pro	Leu	Gly 495
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Cys	Gly	Ile	Pro	Lys 545	His	Phe	Gly	Leu	Phe 550	Tyr	Ala	Met	Gly	Thr 555
Ala	Leu	Met	Met	Glu 560	Gly	Leu	Leu	Ser	Ala 565	Cys	Tyr	His	Val	Cys 570
Pro	Asn	Tyr	Thr	Asn 575	Phe	Gln	Phe	Asp	Thr 580	Ser	Phe	Met	Tyr	Met 585
Ile	Ala	Gly	Leu	Cys 590	Met	Leu	Lys	Leu	Tyr 595	Gln	Lys	Arg	His	Pro 600
Asp	Ile	Asn	Ala	Ser 605	Ala	Tyr	Ser	Ala	Tyr 610	Ala	Cys	Leu	Ala	Ile 615

Val	Ile	Phe	Phe	Ser 620	Val	Leu	Gly	Val	Val 625	Phe	Gly	Lys	Gly	Asn 630
Thr	Ala	Phe	Trp	Ile 635	Val	Phe	Ser	Ile	Ile 640	His	Ile	Ile	Ala	Thr 645
Leu	Leu	Leu	Ser	Thr 650	Gln	Leu	Tyr	Tyr	Met 655	Gly	Arg	Trp	Lys	Leu 660
Asp	Ser	Gly	Ile	Phe 665	Arg	Arg	Ile	Leu	His 670	Val	Leu	Tyr	Thr	Asp 675
Cys	Ile	Arg	Gln	Cys 680	Ser	Gly	Pro	Leu	Tyr 685	Val	Asp	Arg	Met	Val 690
Leu	Leu	Val	Met	Gly 695	Asn	Val	Ile	Asn	Trp 700	Ser	Leu	Ala	Ala	Tyr 705
Gly	Leu	Ile	Met	Arg 710	Pro	Asn	Asp	Phe	Ala 715	Ser	Tyr	Leu	Leu	Ala 720
Ile	Gly	Ile	Cys	Asn 725	Leu	Leu	Leu	Tyr	Phe 730	Ala	Phe	Tyr	Ile	Ile 735
Met	Lys	Leu	Arg	Ser 740	Gly	Glu	Arg	Ile	Lys 745	Leu	Ile	Pro	Leu	Leu 750
Cys	Ile	Val	Cys	Thr 755	Ser	Val	Val	Trp	Gly 760	Phe	Ala	Leu	Phe	Phe 765
Phe	Phe	Gln	Gly	Leu 770	Ser	Thr	Trp	Gln	Lys 775	Thr	Pro	Ala	Glu	Ser 780
Arg	Glu	His	Asn	Arg 785	Asp	Cys	Ile	Leu	Leu 790	Asp	Phe	Phe	Asp	Asp 795
His	Asp	Ile	Trp	His 800	Phe	Leu	Ser	Ser	Ile 805	Ala	Met	Phe	Gly	Ser 810
Phe	Leu	Val	Leu	Leu 815	Thr	Leu	Asp	Asp	Asp 820	Leu	Asp	Thr	Val	Gln 825
Arg	Asp	Lys	Ile	Tyr 830	Val	Phe								

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<210> 228
<211> 2848
<212> DNA
<213> Homo sapiens
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<400> 228
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tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100
ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150
gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200
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tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacctg 250
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350
 ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400
 taccagctac aggtcacccct ggagatgcag gatggacatg tcttgtgggg 450
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550
 ggcatccctc tctcttctct tgaggcttca gaccgggatg agccaggcac 600
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 atcccccgga accctttgaa gtgaatgcag agggaaacct ctacgtgacc 1000
 agagagctgg acagagaagc ccaggctgag tacctgtccc aggtgcgggc 1050
 tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100
 tgggtgatga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150
 acagtacgca tccctgagct cagtccacca ggtactgaag tgactagact 1200
 gtcagcagag gatgcagatg cccccggctc ccccaattcc cacgttgtgt 1250
 atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300
 caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tccactccg 1350
 agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400
 cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450
 atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500
 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550
 ttgatgctga cctcgagccc gccttccgcc tcatggattt tgccattgag 1600
 aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln
1 5 10 15

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20										25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

(Musical notation for the first system of the score)

605	610	615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp
620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu
635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His
650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser
665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val
680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr
695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile Ile
710	715	720
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val
725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg
740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val
755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile
770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp
785	790	795
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val
800	805	

<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
 cgccttaccg cgcagcccgga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aacccactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
 ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
 atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
 acttgaagct caattttctgg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250
 atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
 agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
 cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
 actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
 ttcccgagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
 ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
 atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700
 tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750
 gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
 ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
atgggaatth caagggcttc atcgacctgc acagctactc gcagctgctg 950
atgtatccat atgggtactc agtcaaaaag gccccagatg ccgaggaact 1000
cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050
ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100
agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150
tgagttgaga gataccggga cctatggctt cctcctgccg gctaaccaga 1200
tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250
catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300
atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350
cctacctgtg tgagtcagag ccctctgggt ttgtggagca cacaggcctg 1400
ccctctcca gccagctccc tggagtcgtg tgtcctggcg gtgtccctgc 1450
aagaactggt tctgccagcc tgctcaattt tggctcctgct gtttttgatg 1500
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gatctgtgtc actgtaggta ctgtgccag gaaggctggg tgaagtgacc 2300

.....

atctaaattg caggatgggtg aaattatccc catctgtcct aatgggctta 2350
cctcctcttt gccttttgaa ctcaattcaa agatctagga ctcatttac 2400
aggctcctaaa tcaactcatct ggccctggata atctcactgc cctggcacat 2450
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tottaacctc ctgcctagga tttgtacagc atctgggtgtg tgcttataag 2750
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<210> 234
<211> 421
<212> PRT
<213> Homo sapiens

<400> 234
Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile
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Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
20 25 30
Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
35 40 45
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
50 55 60
Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
65 70 75
Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
80 85 90
Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
95 100 105
Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
110 115 120
Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
125 130 135
Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
140 145 150
His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
155 160 165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
170 175 180

His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
185 190 195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
200 205 210

Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
215 220 225

Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
230 235 240

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
245 250 255

Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
260 265 270

Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
275 280 285

Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
290 295 300

Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
305 310 315

Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
320 325 330

Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
335 340 345

Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
350 355 360

Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
365 370 375

Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
380 385 390

Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
395 400 405

Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
410 415 420

Tyr

<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 235

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 cccgcccttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200
 aacaccgact ttgccttccg cctataccgc aggettggtt tggagacccc 250
 gagtcagaac atctttcttct cccctgtgag tgtctccact tccctggcca 300
 tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350
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 aactggaaca ggccttgta gccagaacac tgataaagtg gagccactca 950
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 ggatgttgct gggttaccat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataaacac 1650
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<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
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 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

<211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 238
 ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 239
 tgactcgggg tctccaaaac cagc 24

<210> 240
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 240
 ggtataggcg gaaggcaaag tcgg 24

<210> 241
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 241
 ggcattcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
 <211> 2436
 <212> DNA
 <213> Homo sapiens

<400> 242
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caactctgac tccagcacia cctccagtga ggccagcaca gccaccaact 1550
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tccagcacia cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650
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ctgggtgccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc 1800
cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850
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gtggagtcct aactgggtct ggaggagacc agtatcatcg atagccatgg 2000
agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050
gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100
cattcatccc aggagacccc tccagcttt gtttgagatc ctgaaaatct 2150
tgaagaaggt attctcacc tttcttgctt ttaccagaca ctggaaagag 2200
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
<211> 596
<212> PRT
<213> Homo sapiens

<400> 243
Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
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20 25 30
Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
35 40 45
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
50 55 60
Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
65 70 75

	365		370		375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala		
	380		385		390
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala		
	395		400		405
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala		
	410		415		420
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala		
	425		430		435
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val		
	440		445		450
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala		
	455		460		465
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala		
	470		475		480
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala		
	485		490		495
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile		
	500		505		510
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe		
	515		520		525
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn		
	530		535		540
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly		
	545		550		555
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro		
	560		565		570
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile		
	575		580		585
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro			
	590		595		

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic sequence.

<400> 245
 gtcagagttg gtggctgtgc tagc 24

<210> 246
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 246
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<210> 247
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 247
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 tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150
 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
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 gaagcagaga agcttggccca tggggtcaac aacgctgctg gacaggccgg 450
 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500
 ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550
 caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 249
caatatgcat cttgcacgtc tgg 23

<210> 250
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 250
aagcttctct gcttcctttc ctgc 24

<210> 251
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 251
tgacccatt gagaaggatca ttgaaggat caaccgagg ctg 43

<210> 252
<211> 3781
<212> DNA
<213> Homo sapiens

<400> 252

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 tgacctgac tcaactccagg tccggaggcg ggggcccccg gggcgactcg 150
 ggggcggacc gcggggcgga gctgcgcgcc gtgagtccgg ccgagccacc 200
 tgagcccag ccgcgggaca ccgtcgtctc tgctctccga atgctgcgca 250
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 gtttttatac attttttaaat aagatgcact ttatgtcatt ttttaataaa 3750
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

80										85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
				95					100					105					
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
				110					115					120					
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
				125					130					135					
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly					
				140					145					150					
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
				155					160					165					
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
				170					175					180					
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala					
				185					190					195					
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
				200					205					210					
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
				215					220					225					
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
				230					235					240					
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
				275					280					285					
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
				290					295					300					
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
				305					310					315					
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
				320					325					330					
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
				335					340					345					
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
				350					355					360					
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys	
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccggtgca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

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 cctgcggggc gctcgggggc cgcgatgggc gcggcgggcc cgcggcggcg 350
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 gccacggcg ccgcgccagc cccgagggt gccgggtccg gcaggcggcg 650
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 gccgcccggc tcggaccag atggcggccc gcgcgacagg aactttctct 750
 tcgtgggagt catgaccgcc cagaaatacc tgcagactcg ggccgtggcc 800
 gcctacagaa catggtccaa gacaattcct gggaaagtgc agttcttctc 850
 aagtgagggt tctgacacat ctgtaccaat tccagtagtg ccactacggg 900
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 gtgggaaggt gtgtccggag gtttgcaggg gtgcagtgtg tctggtctta 1300
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 acattagaga tctccataac agtaaaattc accaagctat cacattacac 1400
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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	20	25	30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	35	40	45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	50	55	60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	65	70	75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	80	85	90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	95	100	105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	110	115	120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	125	130	135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	140	145	150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	155	160	165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	170	175	180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	185	190	195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	200	205	210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	215	220	225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	230	235	240	

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
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<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400


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<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

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320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
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Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
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Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

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gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
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agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

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ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcggt ggtgggacag aagtagaaga ggggtgaatgg ccctggcagg 650
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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

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Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln
185	190	195	
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met
200	205	210	
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe
215	220	225	
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu
230	235	240	
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro
245	250	255	
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His
260	265	270	
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg
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290	295	300	
Glu Met Glu Glu	Leu		
305			

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	185	190	195	
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	200	205	210	
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	215	220	225	
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	230	235	240	
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	245	250	255	

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Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly
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Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr
				20					25					30
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr
				35					40					45
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly
				50					55					60
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr
				65					70					75
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln
				80					85					90
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala
				95					100					105
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn
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Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn
				125					130					135
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala
				140					145					150
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser
				155					160					165
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro
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Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser
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Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg
				200					205					210
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg
				215					220					225
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr
				230					235					240
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp
				245					250					255
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys
				260					265					270
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr
				275					280					285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
ctgctgggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
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<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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 tgtgcttgag agttcagggc cggacacagg ctacacaggtc tccacattgg 2200
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<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

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Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
          20          25          30
Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
          35          40          45
Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
          50          55          60
Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
          65          70          75
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
          80          85          90
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
          95          100          105
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
          110          115          120
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
          125          130          135
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
          140          145          150
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
          155          160          165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
          170          175          180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
          185          190          195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
          200          205          210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
          215          220          225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
          230          235          240
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
          245          250          255
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

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<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggg ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
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 gtgtgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 287
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
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 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
 20 25 30
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn
 80 85 90
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
 95 100 105
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
 110 115 120
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
 125 130 135
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
 140 145 150
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
 155 160 165
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292
 Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
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 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
 20 25 30
 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180
 Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
 185 190 195
 Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
 200 205 210
 Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
 215 220 225
 Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
 230 235 240
 Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
 245 250 255
 Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
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<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 295
 aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
 <211> 3060
 <212> DNA
 <213> Homo sapiens

<400> 296
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aaaaccacct	gattcaaaaat	gggcagaggg	gccgggtgtg	gccccaaacta	2950
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<210> 297
<211> 368
<212> PRT
<213> Homo sapiens
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<400> 297														
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Leu	Val	Gly	Phe	Val 20	Phe	Val	Val	Ser	Gly 25	Leu	Val	Ile	Asn	Phe 30
Val	Gln	Leu	Cys	Thr 35	Leu	Ala	Leu	Trp	Pro 40	Val	Ser	Lys	Gln	Leu 45
Tyr	Arg	Arg	Leu	Asn 50	Cys	Arg	Leu	Ala	Tyr 55	Ser	Leu	Trp	Ser	Gln 60
Leu	Val	Met	Leu	Leu 65	Glu	Trp	Trp	Ser	Cys 70	Thr	Glu	Cys	Thr	Leu 75
Phe	Thr	Asp	Gln	Ala 80	Thr	Val	Glu	Arg	Phe 85	Gly	Lys	Glu	His	Ala 90
Val	Ile	Ile	Leu	Asn 95	His	Asn	Phe	Glu	Ile 100	Asp	Phe	Leu	Cys	Gly 105
Trp	Thr	Met	Cys	Glu 110	Arg	Phe	Gly	Val	Leu 115	Gly	Ser	Ser	Lys	Val 120
Leu	Ala	Lys	Lys	Glu 125	Leu	Leu	Tyr	Val	Pro 130	Leu	Ile	Gly	Trp	Thr 135
Trp	Tyr	Phe	Leu	Glu 140	Ile	Val	Phe	Cys	Lys 145	Arg	Lys	Trp	Glu	Glu 150
Asp	Arg	Asp	Thr	Val 155	Val	Glu	Gly	Leu	Arg 160	Arg	Leu	Ser	Asp	Tyr 165

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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 tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
 cggccctggg ttagaaggga aggaagata aacttttata caaatgggga 250
 tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
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 gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
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 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggata 600
 ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650
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140

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

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<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
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 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

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ccggctctcc	gtgcccgcg	cgctggccct	gggctcagcc	gcactgggcg	150
ccgccttcgc	cactggcctc	ttcctgggga	ggcggtgccc	cccatggcga	200
ggccggcgag	agcagtgcct	gcttcccccc	gaggacagcc	gcctgtggca	250
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caggcccagc	tcttgccaa	cctggcgcg	ctcatccagg	ccaagaaggc	400
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ccggagctgg	gacggcccct	gtggaggcag	gccgaggcgg	agcacaagat	550
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<210> 306
<211> 262
<212> PRT
<213> Homo sapiens
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<400> 306
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Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
          20          25          30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
          35          40          45

Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
          50          55          60

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Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

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<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308
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Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser
155		160	165
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala
170		175	180
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu
185		190	195
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala
200		205	210
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys
215		220	225
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser
230		235	240
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser
245		250	255
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val
260		265	270
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro
275		280	285
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser
290		295	300
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu
305		310	315
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg
320		325	330
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln
335		340	345
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly
350		355	360
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg
365		370	375
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly
380		385	390
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu
395		400	405
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser
410		415	420
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg
425		430	435

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80					85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
				230					235					240
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu
				260					265					270
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
				275					280					285
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
				290					295					300
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
				305					310					315
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
				320					325					330
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335					340					345
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
				350					355					360
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His
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[illegible]

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<211> 3934
<212> DNA
<213> Homo sapiens

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Val Phe Pro Pro Thr Pro Val Leu Cys Leu Pro Asn Gln Val Leu
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Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
35 40 45

Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
50 55 60

Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
65 70 75

Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
80 85 90

Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
95 100 105

Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
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Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
125 130 135

Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
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Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
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Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
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Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
185 190 195

Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
200 205 210

Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
215 220 225

Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
230 235 240

Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
245 250 255

Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
260 265 270

Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
275 280 285

Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
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Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala

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Pro Thr Ser Val Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro Gly	
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro	
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 <211> 4407
 <212> DNA
 <213> Homo sapiens

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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
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35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
 440 445 450
 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
 500 505 510
 Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
 515 520 525
 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
 530 535 540
 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
 605 610 615
 Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
 695 700 705
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

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Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys	830		835		

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
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<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cgggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320

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<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

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Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

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<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324
Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
1 5 10 15
Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
20 25 30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
35 40 45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
50 55 60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
80 85 90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
95 100 105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
110 115 120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
125 130 135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
140 145 150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
155 160 165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
170 175 180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
185 190 195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
200 205 210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgctca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
 gtccctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500
 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 ggggggtgtga tgatgtgcat cgctgccgg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
 tccttccaag cagactatg tgtaatgtc taagacctct cagcacgggc 900
 ggaagaaact ccgggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cgggttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcggggc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
				245					250					255					
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgcgt 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaac caaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaaact ttgatttact gttcttaact gcctaattctt aattacagga 900
 actgtgcacg agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taagggtggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctccataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaagggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagagggt ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatatt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

gccccctcg tctaccccc tttaactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu	1	5	10	15
Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp	20	25	30	
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val	35	40	45	
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly	50	55	60	
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val	80	85	90	
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr	95	100	105	
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr	110	115	120	
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro	125	130	135	
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr	155	160	165	
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu	170	175	180	
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His	185	190	195	
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly	200	205	210	
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val	215	220							

<210> 331

<211> 1160

<212> DNA

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctcaaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

ttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgccgcca tggctgcctc ccccgcgcgq cctgctgtcc 100

tgccctgac cgggctggcg ctgctcctgc tctgtgctg qggcccaagt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgagggtgc agcagtggtta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctagggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcatgtatc tcctaatgcc ttacactact tggttttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagaggttaa aacaacacat gtaaatgcct ttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
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agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgctc agggaccca acgcatccc agccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
 ggggttcacag caacaccgcc agccccggac tccccgcagg agccccctgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcagggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcgggtccc ccaaatcccc cctgcccgcc ggggtccgag 650
 cccggccccct ccggggtgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttcccttgac cgccactctg ggcttgccg gcttcaccct gtcctcagt 800
 ctctggcct ttgccatgta ccgccgtag tgctccgcg ggcgcttggc 850
 agcgtgcgcg gcccctccgg accttgctcc ccgcgcgcg gcgggagctg 900
 ctgcctgcc aggccgcct ctccggcctg cctcttcccg ctgccctgga 950
 gccagccct gcgcgcgaga ggactcccgg gactggcgga ggccccgcc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgcactggga gtgggtcctt cggggctcgg catctgctgt cgctgcctcg 1100
 gccccgggca gagccgggccc gccccggggg cccgtcttag tgttctgccg 1150
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 acgccaggtc ggtgggaggc tggatgaagg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
 aaaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 5 10 15
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
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 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacccta agaaccatca gccctcagct gcacctctc ccctccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

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aggaacttgga tgggtttgag ggttactccc tgagtgaactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaatggagg ttgcaactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
tcttggttc ctccttactc ccatctggac ccagtcacct ggttcctgtc 800
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
  1           5           10
Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
          20           25
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
          35           40
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
          50           55
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
          65           70
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
          80           85
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
          95          100
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
          110          115
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
          125          130
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

```

145

```
<210> 341
<211> 23
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.
```

<400> 341
ccctccaagg atgacaaagg cgc 23

```
<210> 342
<211> 29
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.
```

```
<400> 342
ggtcagcagc tttcttgccc taaatcagg 29
```

```
<210> 343
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 343
  atctcaggcg gcatcctgtc agcc 24
```

```
<210> 344
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 344
gtggatgcct gcaagaaggt tggg 24
```

```
<210> 345
<211> 45
<212> DNA
<213> Artificial
```


<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 345
 agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

 <210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

 <400> 346
 tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
 actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
 caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
 aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
 gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
 ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggctc 300
 ttgcacacgc tgttggaaca tgtcaggacc aggttaagtg actggcagaa 350
 aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
 gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450
 gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
 ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
 ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
 aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650
 tcccaggatt gggtagtgga agctgaggat gaggggtgaag agtacagccc 700
 tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
 tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800
 ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
 cccaaagagg gactgggggg ctgatgagga cggggagggtg tctgaagaag 900
 aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950
 agtggccgca tccccctcca gagggctctg cccgagggtgc ggcaccact 1000
 gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
 tctgtttcca tgatgaggcc tgggtccaact tctgcggaac tgtacacagc 1100

atcctcgaca cagtgccag ggccttcctg aaggagatca tcctcgtgga 1150
 cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200
 ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250
 atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300
 cttcatggat gccactgcg agtgccaccc aggctggctg gagccccctcc 1350
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 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
 tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
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 gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600
 agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctggaactgt 1650
 ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700
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 ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggctggggt 1800
 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
 acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000
 cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050
 catggtgttg gtccttgca gtgacagccg gcagcaacag tacctgcagc 2100
 acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150
 gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200
 ggccatccac cagcagcact gggaactcca ggagaatggg atgattgtcc 2250
 acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300
 gatttgtacc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350
 tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400
 aagagaatth tggccatcaa aatccagctc caagtgaacg taaagagctt 2450
 atatatttca tgaagctgat ccttttgtgt gtgtgctcct tgtgttagga 2500
 gagaaaaaag ctctatgaaa gaatatagga agtttctcct tttcacacct 2550

545										550					555				
Gly	Ser	Pro	Gln	His 560	Leu	Cys	Phe	Ala	Val 565	Arg	Gln	Glu	Gln	Val 570					
Ile	Leu	Gln	Asn	Cys 575	Thr	Glu	Glu	Gly	Leu 580	Ala	Ile	His	Gln	Gln 585					
His	Trp	Asp	Phe	Gln 590	Glu	Asn	Gly	Met	Ile 595	Val	His	Ile	Leu	Ser 600					
Gly	Lys	Cys	Met	Glu 605	Ala	Val	Val	Gln	Glu 610	Asn	Asn	Lys	Asp	Leu 615					
Tyr	Leu	Arg	Pro	Cys 620	Asp	Gly	Lys	Ala	Arg 625	Gln	Gln	Trp	Arg	Phe 630					
Asp	Gln	Ile	Asn	Ala 635	Val	Asp	Glu	Arg											

```
<210> 348
<211> 23
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.
```

```
<400> 348
ggagaggtgg tggccatgga cag 23
```

<210>	349
<211>	24
<212>	DNA
<213>	Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

```
<400> 349
ctgtcactgc aaggagccaa cacc 24
```

<210>	350
<211>	45
<212>	DNA
<213>	Artificial

```
<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.
```

```
<400> 350
  tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaqgc 45
```

338

ccaagcagga	ggccaagggg	ccggcacagc	ccccatccca	ctgagggtgg	1350
ggcagctgtg	gggagctggg	gccacagggg	ctcctggctc	ctgccccttg	1400
cacaccaccc	ggaacactcc	ccagccccac	gggcaatcct	atctgctcgc	1450
cctcctgcag	gtgggggcct	cacatatctg	tgacttcggg	tcctgtgcc	1500
cacccttgtg	cactcacatg	aaagccttgc	acactcacct	ccaccttcac	1550
aggccatttg	cacacgctcc	tgcaccctct	ccccgtccat	accgctccgc	1600
tcagctgact	ctcatgttct	ctcgtctcac	atttgactc	tctccttccc	1650
acattctgtg	ctcagctcac	tcagtgggtca	gcgtttcctg	cacactttac	1700
ctctcatgtg	cgtttcccg	cctgatgttg	tggtgggtg	cggcgtgctc	1750
actctctccc	tcatgaacac	ccaccacct	cgtttccgca	gccctgcgt	1800
gctgctccag	aggtgggtgg	gaggtgagct	gggggctcct	tgggccctca	1850
tcggtcatgg	tctcgtccca	ttccacacca	ttgtttctc	tgtctcccca	1900
tcctactcca	aggatgccgg	catcacccctg	agggctcccc	cttgggaatg	1950
gggtagtgag	gccccagact	tcacccccag	cccactgcta	aaatctgttt	2000
tctgacagat	gggttttggg	gagtcgcctg	ctgcactaca	tgagaaaggg	2050
actcccattt	gcccttccct	ttctcttaca	gtcccttttg	tcttgtctgt	2100
cctggctgtc	tgtgtgtgtg	ccattctctg	gacttcagag	cccctgagc	2150
cagtcctccc	ttcccagcct	ccctttgggc	ctccctaact	ccacctaggc	2200
tgccagggac	cggagtcagc	tggttcaagg	ccatcgggag	ctctgcctcc	2250
aagtctaccc	ttcccttccc	ggactccctc	ctgtcccctc	ctttcctccc	2300
tccttccttc	cactctcctt	ccttttgctt	cctgcccctt	ttcccctcct	2350
caggttcttc	cctccttctc	actggttttt	ccaccttcct	ccttccccttc	2400
ttccctggct	cctaggctgt	gatatatatt	tttgtattat	ctctttcttc	2450
ttcttgtggt	gatcatcttg	aattactgtg	ggatgtaagt	ttcaaaattt	2500
tcaaaataaag	cctttgcaag	ataa	2524		

```
<210> 352
<211> 243
<212> PRT
<213> Homo sapiens
```

<400> 352
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15

Leu	Leu	Leu	Leu	Leu 20	Leu	Leu	Gln	Leu	Pro 25	Ala	Pro	Ser	Ser	Ala 30
Ser	Glu	Ile	Pro	Lys 35	Gly	Lys	Gln	Lys	Ala 40	Gln	Leu	Arg	Gln	Arg 45
Glu	Val	Val	Asp	Leu 50	Tyr	Asn	Gly	Met	Cys 55	Leu	Gln	Gly	Pro	Ala 60
Gly	Val	Pro	Gly	Arg 65	Asp	Gly	Ser	Pro	Gly 70	Ala	Asn	Val	Ile	Pro 75
Gly	Thr	Pro	Gly	Ile 80	Pro	Gly	Arg	Asp	Gly 85	Phe	Lys	Gly	Glu	Lys 90
Gly	Glu	Cys	Leu	Arg 95	Glu	Ser	Phe	Glu	Glu 100	Ser	Trp	Thr	Pro	Asn 105
Tyr	Lys	Gln	Cys	Ser 110	Trp	Ser	Ser	Leu	Asn 115	Tyr	Gly	Ile	Asp	Leu 120
Gly	Lys	Ile	Ala	Glu 125	Cys	Thr	Phe	Thr	Lys 130	Met	Arg	Ser	Asn	Ser 135
Ala	Leu	Arg	Val	Leu 140	Phe	Ser	Gly	Ser	Leu 145	Arg	Leu	Lys	Cys	Arg 150
Asn	Ala	Cys	Cys	Gln 155	Arg	Trp	Tyr	Phe	Thr 160	Phe	Asn	Gly	Ala	Glu 165
Cys	Ser	Gly	Pro	Leu 170	Pro	Ile	Glu	Ala	Ile 175	Ile	Tyr	Leu	Asp	Gln 180
Gly	Ser	Pro	Glu	Met 185	Asn	Ser	Thr	Ile	Asn 190	Ile	His	Arg	Thr	Ser 195
Ser	Val	Glu	Gly	Leu 200	Cys	Glu	Gly	Ile	Gly 205	Ala	Gly	Leu	Val	Asp 210
Val	Ala	Ile	Trp	Val 215	Gly	Thr	Cys	Ser	Asp 220	Tyr	Pro	Lys	Gly	Asp 225
Ala	Ser	Thr	Gly	Trp 230	Asn	Ser	Val	Ser	Arg 235	Ile	Ile	Ile	Glu	Glu 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50

cggccaggat ggcatacctgt ctggccctgc gcatggcgct gctgctggtc 100


```
tccggggttc tggccccctgc ggtgctcaca gacgatgttc cacaggagcc 150
cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
ccgtggagag caccagcccc ggccgggagc ccgtggacac cgggtcccca 250
gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
ggaccagggc ggcgggctgc tggggcccgg cgctatcgcg gccatcgtga 350
tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
ctgagaaaagt tttctgcctc ctgaagcgaa taaagggggc gcgcccggcc 450
gcggcgcgac tcggcaaaaa aaaaaaaaaa 480
```

```
<210> 354
<211> 121
<212> PRT
<213> Homo sapiens
```

[illegible]

```
<210> 355
<211> 2134
<212> DNA
<213> Homo sapiens
```

```
<400> 355
ggccggttggt tgggtgcgcgg ctgaaggggtg tggcgcgagc agcgtcgttg 50
gttggccggc ggcggggccgg gacggggcatg gccctgctgc tgtgacctggt 100
```

gtgcctgacg	gcggcgctgg	cccacggctg	tctgactg	cacagcaact	150
tctccaagaa	gttctccttc	taccgccacc	atgtgaactt	caagtcttgg	200
tgggtggg	acatccccgt	gtcagggg	ctgctcaccg	actggagcga	250
cgacacgatg	aaggagctgc	acctggccat	ccccgccaa	atcacccggg	300
agaagctgga	ccaagtggcg	acagcagtgt	accagatgat	ggatcagctg	350
taccagggga	agatgtactt	ccccgggtat	ttccccaacg	agctgcgaaa	400
catcttccgg	gagcaggtgc	acctcatcca	gaacgccatc	atcgaaaggc	450
acctggcacc	aggcagctgg	ggaggagggc	agctctccag	ggagggaccc	500
agcctagcac	ctgaaggatc	aatgccatca	ccccgcgggg	acctccccta	550
agtagcccc	agaggcgctg	ggagtgttgc	caccgccttc	ccctgaagtt	600
tgtccatct	cacgctgggg	gtcaacctgg	ggacccttc	cctccggg	650
atggacacac	atacatgaaa	accaggccgc	atcgactgtc	agcaccgctg	700
tggcatcttc	cagtacgaga	ccatctcctg	caacaactgc	acagactcgc	750
acgtcgctg	ctttggctat	aactgcgagt	agggctcagg	catcacacc	800
acccgtgcca	gggccctact	gtccctgggg	tcccaggctc	tccttgagg	850
gggctccccg	ccttcacact	ggctgtcatc	gggtagggcg	gggccgtggg	900
ttcagggg	caccacttcc	aagcctgtgt	cccacaggtc	ctcggcgcag	950
tggaagtcag	ctgtccaggg	cctcctgaac	tacataaata	actggcacia	1000
gtaagtcccc	tcctcaaacc	aacacaggca	gtgtgtgtat	gtgagcacct	1050
cgtgggtgag	tatgtgtggg	gcacaggctg	gctccctcag	ctcccacgtc	1100
ctagagggg	tcccaggagg	gtggaacctc	aaccagctc	tgcgcaggag	1150
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cgggcatctt	tcctaaagg	tcccatagg	gtctggttcc	accccatccc	1250
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ccatggagg	gctgactgcc	ccacattgcc	tttcagacag	gacacgagca	1350
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agaggagggg	ggctagggg	tcctctagat	cagtgggggc	actgcaggtg	1450
gggctctccc	tatacctggg	acacctgctg	gatgtcacct	ctgcaaccac	1500
acccatgtgg	tggtttcatg	aacagaccac	gtcctctctg	cttctcctgg	1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
 cataggacca cacgtcccag ctgggaggag aggcctgggg ccccaggga 1750
 gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
 gctgggcctg cccagggga acgtgggggc ggagactcag ctggacagcc 1950
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg acccctctc 2000
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt cctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Ala Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1 5 10 15
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
 125 130 135
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatggt 50
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatggt cctggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctcctga taatgaacaa ggcctccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggatgaaa gaaaatggga aggtgatatc 650
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 359
ccagcagtgcc ccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 360
tgacgagtggt gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcgcggcgcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggctcgg gctggcgcg gcgcttgggc 250
tcttgacagc tggagtatca gccttgggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcggttgga cctcagcttc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgttt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gtttagaccac 900
tccggcgga atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac	caaactggac	tctcgtgcag	aaaatgtagc	ccattaccac	1050
atgtagcctt	ggagaccacg	gcaaggacaa	gtacacgtgt	actcacagag	1100
ggagagaaaag	atgtgtacaa	aggatatgta	taaatattct	atttagtcac	1150
cctgatatga	ggagccagtg	ttgcatgatg	aaaagatggg	atgattctac	1200
atatgtaccc	attgtcttgc	tgtttttgta	ctttcttttc	aggtcattta	1250
caattgggag	atttcagaaa	cattcctttc	accatcattt	agaaatgggt	1300
tgcccttaatg	gagacaatag	cagatccctgt	agtattttcca	gtagacatgg	1350
cctttttaatc	taagggctta	agactgatta	gtcttagcat	ttactgtagt	1400
tggaggatgg	agatgctatg	atggaagcat	accagggtg	gccttttagca	1450
cagtatcagt	accattttatt	tgtctgccgc	ttttaaaaaa	taccatttgg	1500
ctatgccact	tgaaaacaat	ttgagaagtt	tttttgaagt	ttttctcact	1550
aaaatatggg	gcaattgtta	gccttacatg	ttgtgtagac	ttacttttaag	1600
tttgaccct	tgaaatgtgt	catatcaatt	tctggattca	taatagcaag	1650
attagcaaag	gataaatgcc	gaaggctcact	tcattctgga	cacagttgga	1700
tcaatactga	ttaagtagaa	aatccaagct	ttgcttgaga	acttttgtaa	1750
cgtggagagt	aaaaagtatc	ggtttta	1777		

```
<210> 364
<211> 269
<212> PRT
<213> Homo sapiens
```

```

<400> 364
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1          5          10          15

Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
          20          25          30

Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
          35          40          45

Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
          50          55          60

Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
          65          70          75

Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
          80          85          90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
          95          100          105

```


Arg	Ile	Ser	Trp	Ala 110	Gly	Asp	Leu	Asp	Lys 115	Lys	Asp	Ala	Ser	Ile 120
Asn	Ile	Glu	Asn	Met 125	Gln	Phe	Ile	His	Asn 130	Gly	Thr	Tyr	Ile	Cys 135
Asp	Val	Lys	Asn	Pro 140	Pro	Asp	Ile	Val	Val 145	Gln	Pro	Gly	His	Ile 150
Arg	Leu	Tyr	Val	Val 155	Glu	Lys	Glu	Asn	Leu 160	Pro	Val	Phe	Pro	Val 165
Trp	Val	Val	Val	Gly 170	Ile	Val	Thr	Ala	Val 175	Val	Leu	Gly	Leu	Thr 180
Leu	Leu	Ile	Ser	Met 185	Ile	Leu	Ala	Val	Leu 190	Tyr	Arg	Arg	Lys	Asn 195
Ser	Lys	Arg	Asp	Tyr 200	Thr	Gly	Cys	Ser	Thr 205	Ser	Glu	Ser	Leu	Ser 210
Pro	Val	Lys	Gln	Ala 215	Pro	Arg	Lys	Ser	Pro 220	Ser	Asp	Thr	Glu	Gly 225
Leu	Val	Lys	Ser	Leu 230	Pro	Ser	Gly	Ser	His 235	Gln	Gly	Pro	Val	Ile 240
Tyr	Ala	Gln	Leu	Asp 245	His	Ser	Gly	Gly	His 250	His	Ser	Asp	Lys	Ile 255
Asn	Lys	Ser	Glu	Ser 260	Val	Val	Tyr	Ala	Asp 265	Ile	Arg	Lys	Asn	

```
<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens
```

```
<400> 365
gccggctgtg cagagacgcc atgtaccggc tctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100
ccatcagcgc gccgggctgc cgctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
agaccccggc gccgccctgc tccagggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcy caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tgttgagaac cgtgtaccat gtaaacaga gacagttatg 500
```

cgaattgcta	gcatcagcaa	aagtctcacc	atggttgctc	ttgccaaatt	550
gtgggaagca	gggaaactgg	atcttgatat	tccagtacaa	cattatgttc	600
ccgaattccc	agaaaaagaa	tatgaagggtg	aaaaggtttc	tgtcacaaca	650
agattactga	tttcccattt	aagtggaatt	cgtcattatg	aaaaggacat	700
aaaaaagggtg	aaagaagaga	aagcttataa	agccttgaag	atgatgaaag	750
agaatgttgc	atttgagcaa	gaaaaagaag	gcaaaagtaa	tgaaaagaat	800
gattttacta	aatttaaaac	agagcaggag	aatgaagcca	aatgccggaa	850
ttcaaaacct	ggcaagaaaa	agaatgattt	tgaacaaggc	gaattatatt	900
tgagagaaaa	gtttgaaaat	tcaattgaat	ccctaagatt	atttaaaaat	950
gatcctttgt	tcttcaaacc	tggtagtcag	tttttgtatt	caacttttgg	1000
ctatacccta	ctggcagcca	tagtagagag	agcttcagga	tgtaaataatt	1050
tggactatat	gcagaaaata	ttccatgact	tggatatgct	gacgactgtg	1100
caggaagaaa	acgagccagt	gatttacaat	agagcaaggt	aaatgaatac	1150
cttctgctgt	gtctagctat	atcgcatctt	aacactattt	tattaattaa	1200
aagtcaaatt	ttctttgttt	ccattccaaa	atcaacctgc	cacatttttg	1250
gagcttttct	acatgtctgt	tttctcatct	gtaaaagtga	ggaagtaaaa	1300
catgtttata	aagtaaaaaa	a	1321		

```
<210> 366
<211> 373
<212> PRT
<213> Homo sapiens
```

```

<400> 366
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1          5          10          15
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
          20          25          30
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
          35          40          45
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
          50          55          60
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
          65          70          75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
          80          85          90

```

<210> 367

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccggggc gggactggtg cgcgaggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctggtg gctatgtctc ctcccttctc cctgcgtgct ccctggtgga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372
<211> 269
<212> PRT
<213> Homo sapiens

<400> 372
Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15
Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30
Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

ctctgtgtta ctccatttta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

ccttgcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggatgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500
gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgcccc cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
tttgggcggt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
cccaggggcc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
cccagggtct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376
<211> 188
<212> PRT
<213> Homo sapiens

<400> 376
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
1 5 10 15
Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
20 25 30
Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
35 40 45
Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
50 55 60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
65 70 75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
95 100 105
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
110 115 120
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
125 130 135
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
140 145 150
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
155 160 165
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
170 175 180
Leu Gln Pro Pro Trp Thr Phe Trp
185

<210> 377
<211> 496
<212> DNA
<213> Artificial

<220>
<221> unsure
<222> 396
<223> unknown base

<400> 377
tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
ctgaacaaga tggtaagca agtgactggg aaaatgcccc tcctctccta 150
ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
atgccacgga ctggtgtctgc cagacccatg actgctgcta tgaccacctg 250
aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
<211> 116
<212> PRT
<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15
Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30
Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45
Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60
Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75
Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90
His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105
Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 379
ctgcctccac tgctctgtgc tggg 24

<210> 380
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 380
cagagcagtg gatgttcccc tggg 24

<210> 381
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75
Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90
Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105
Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120
Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150
Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165
Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttcctggg 400
tgtcagcgag ccctgactca ctacagtgc gctgacaggg gctgtcatgc 450
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatatctgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
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aacctggaac ttttgacctt gggatataac cggatccgaa gtttagccag 1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250
gtcctggacc tggagctcct tacaaaggct tgatttatca ggcaatgaga 1300
tcgaagcttt cagtggaccc agtggtttcc agtgtgtccc gaatctgcag 1350
cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
aatgcagcag aaatatattgc tcccttgtaa actggctgaa aagttttaaa 1500
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaaagta 1600
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700
ggtgggagcc acagagcccc gccagagac cgatgctgac gccgagcaca 1750
tctctttcca taaaatcacc gcgggcagcg tggcgctttt cctgtccgtg 1800
ctcgtcatcc tgctgggtat ctacgtgtca tgggaagcgg accctgagag 1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac agggaaaaga 1900
aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
gggaccctgc acctataaca aatcgggtc cagggagtgt gaggtatgaa 2050
ccatttgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca agggaaacgcg atgccccccc tccccctccc 2150
tctccctctc actttggtgg caagatcctt ccttggtccgt tttagtgcac 2200
tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
<211> 513
<212> PRT
<213> Homo sapiens

<400> 385
Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
1 5 10 15
Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
20 25 30
Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
35 40 45
Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
50 55 60
Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
65 70 75
Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
80 85 90
Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
95 100 105
Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
110 115 120
Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
125 130 135
Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
140 145 150
Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
155 160 165
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
170 175 180
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
185 190 195
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

				200						205					210
His	Leu	Glu	His	Asn 215	Gln	Phe	Ser	Lys	Leu 220	Asn	Leu	Ala	Leu	Phe 225	
Pro	Arg	Leu	Val	Ser 230	Leu	Gln	Asn	Leu	Tyr 235	Leu	Gln	Trp	Asn	Lys 240	
Ile	Ser	Val	Ile	Gly 245	Gln	Thr	Met	Ser	Trp 250	Thr	Trp	Ser	Ser	Leu 255	
Gln	Arg	Leu	Asp	Leu 260	Ser	Gly	Asn	Glu	Ile 265	Glu	Ala	Phe	Ser	Gly 270	
Pro	Ser	Val	Phe	Gln 275	Cys	Val	Pro	Asn	Leu 280	Gln	Arg	Leu	Asn	Leu 285	
Asp	Ser	Asn	Lys	Leu 290	Thr	Phe	Ile	Gly	Gln 295	Glu	Ile	Leu	Asp	Ser 300	
Trp	Ile	Ser	Leu	Asn 305	Asp	Ile	Ser	Leu	Ala 310	Gly	Asn	Ile	Trp	Glu 315	
Cys	Ser	Arg	Asn	Ile 320	Cys	Ser	Leu	Val	Asn 325	Trp	Leu	Lys	Ser	Phe 330	
Lys	Gly	Leu	Arg	Glu 335	Asn	Thr	Ile	Ile	Cys 340	Ala	Ser	Pro	Lys	Glu 345	
Leu	Gln	Gly	Val	Asn 350	Val	Ile	Asp	Ala	Val 355	Lys	Asn	Tyr	Ser	Ile 360	
Cys	Gly	Lys	Ser	Thr 365	Thr	Glu	Arg	Phe	Asp 370	Leu	Ala	Arg	Ala	Leu 375	
Pro	Lys	Pro	Thr	Phe 380	Lys	Pro	Lys	Leu	Pro 385	Arg	Pro	Lys	His	Glu 390	
Ser	Lys	Pro	Pro	Leu 395	Pro	Pro	Thr	Val	Gly 400	Ala	Thr	Glu	Pro	Gly 405	
Pro	Glu	Thr	Asp	Ala 410	Asp	Ala	Glu	His	Ile 415	Ser	Phe	His	Lys	Ile 420	
Ile	Ala	Gly	Ser	Val 425	Ala	Leu	Phe	Leu	Ser 430	Val	Leu	Val	Ile	Leu 435	
Leu	Val	Ile	Tyr	Val 440	Ser	Trp	Lys	Arg	Tyr 445	Pro	Ala	Ser	Met	Lys 450	
Gln	Leu	Gln	Gln	Arg 455	Ser	Leu	Met	Arg	Arg 460	His	Arg	Lys	Lys	Lys 465	
Arg	Gln	Ser	Leu	Lys 470	Gln	Met	Thr	Pro	Ser 475	Thr	Gln	Glu	Phe	Tyr 480	
Val	Asp	Tyr	Lys	Pro 485	Thr	Asn	Thr	Glu	Thr 490	Ser	Glu	Met	Leu	Leu 495	

365

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttgggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tctgtctgct gggttttggtg 250
gcagctcttc tctgtggagc tgtggctcctc tgcctccagt gctggctgag 300
gagaccccca attgattctc acaggcgcac catggcagtt tttgctgttg 350
gagacttggg ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgtctcc 450
atgttttggc ccttttaggt cccacactcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaaagaat 650
ggatgttggg aaaaattttg gtcattggaga tgtttaaata gttaaagtagc 700
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
tctgctttta actctttcct agcatggggg ccataaaaaat tattataatt 900
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcattttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcatttttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1					5				10					15

aagcagatag	gtgagttttt	tataaatctt	ttgtgtttga	gatcaagctg	1150
aatgaaaac	actgaaaaac	atggattcat	ttctataaca	catttattta	1200
agtatataac	acgtttttt	gacaagtga	gaatgtttta	tcattctgtc	1250
atttgttctc	aatagatgta	actgttagac	tacggctatt	tgaaaaaatg	1300
tgcttattgt	actatatttt	gttattccaa	ttatgagcag	agaaaggaaa	1350
tataatgttg	aaaataatgt	tttgaaatca	tgacccaaag	aatgtattga	1400
tttgcactat	ccttcagaat	aactgaaggt	taattattgt	atatttttaa	1450
aaattacact	tataagagta	taatcttgaa	atgggtagca	gccactgtcc	1500
attacctatc	gtaaacattg	gggcaattta	ataacagcat	taaaatagtt	1550
gtaaaactcta	atcttatact	tattgaagaa	taaaagatat	ttttatgatg	1600
agagtaacaa	taaagtattc	atgatttttc	acatacatga	atgttcattt	1650
aaaagttaa	tcctttgagt	gtctatgcta	tcaggaaagc	acattatttc	1700
catatttggg	ttaattttgc	ttttattata	ttggtctagg	aggaagggac	1750
tttggagaat	ggaactcttg	aggactttag	ccaggtgtat	ataataaagg	1800
tacttttgtg	ctgcattaaa	ttgcttgga	agtgttaaca	ttatattata	1850
taagagtatc	ctttatgaaa	ttttgaattt	gtataacaga	tgcathtagat	1900
attcatttta	tataatggcc	acttaaaaata	agaacattta	aaatataaac	1950
tatgaagatt	gactatcttt	tcaggaaaaa	agctgtatat	agcacaggga	2000
accctaattc	tgggtaattc	tagtataaaa	caaattatac	ttttatttaa	2050
atttcccttg	tagcaaatct	aattgccaca	tggtgcccta	tatttcatag	2100
tatttattct	ctatagtaac	tgcttaagtg	cagctagctt	ctagatttag	2150
actatataga	atttagatat	tgtattgttc	gtcattataa	tatgctacca	2200
catgtagcaa	taattacaat	attttattaa	aataaatatg	tgaaatattg	2250
tttcatgaaa	gacagatttc	caaatctctc	ttctcttctc	tgtactgtct	2300
acctttatgt	gaagaaatta	attatatgcc	attgccaggt		2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
1 5 10 15

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
atgggaaccc tctagctgtc attgggtccg gtgccttcgc ggggctggga 750
ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800
gcccagtggc ttccgtgagc taccgggcct gcaggctcctg gacctgtcgg 850
gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900
tccctgcagg agctggacct ttcgggcacc aacctggtgc ccctgcctga 950
ggcgctgtc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000
atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050
ggctccagcc ccaagggtgc cctgcactgc gtagacaccc gggaatctgc 1100
tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150
aacagactgc tgtcctgggc tgctcaggt cccgagtaac ttatgttcaa 1200
tgtgccaaac ccagtgggga gcccgcaggc ctatgtggca gcgtcaccac 1250
aggagtgtg ggcctaggag aggccttggc cctgggagcc acacctagga 1300
gcaaagtctc acccctttgt ctacgttgct tcccaaacc atgagcagag 1350
ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400
cttatcccc aagtgccttc cctcatgcct gggccggcct gacccgcaat 1450
gggcagaggg tgggtgggac ccctgctgc agggcagagt tcaggtccac 1500
tgggctgagt gtccccttgg gcccatggcc cagtcaactca ggggcgagtt 1550
tcttttctaa catagccctt tctttgcat gaggccatga ggcccgttc 1600
atccttttct atttcctag aaccttaatg gtagaaggaa ttgcaaagaa 1650
tcaagtccac ctttctcatg tgacagatgg ggaaactgag gccttgagaa 1700
ggaaaaaggc taatctaagt tcctgcgggc agtggcatga ctggagcaca 1750
gcctcctgcc tcccagccc gacccaatgc actttcttgt ctctctaat 1800
aagccccacc ctccccgcct gggctcccct tgctgccctt gcctgttccc 1850
cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950
ttcggagcct ctggaagctt agggcacatt ggttccagcc tagccagttt 2000
ctcacctgg gttgggtcc ccagcatcc agactggaaa cctaccatt 2050
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gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150
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ggagacaagg tctgcccagc ccatgtctat gctctacccc cagggcagca 2250
tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaaag 2300
ttgttgccct tttaacggag tgtcactttc aaccggcctc ccctaccct 2350
gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400
tttgttcaact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450
aagctgggca tcagtggcca catgggcac caggggctggc cccacagaga 2500
ccccacaggg cagtgaagtc tgtcttcccc cacctgccta gccatcatc 2550
tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397
Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
20 25 30
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
35 40 45
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
50 55 60
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
65 70 75
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
80 85 90
Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
95 100 105
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
110 115 120
Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
125 130 135
Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
 155 160 165
 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
 170 175 180
 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
 185 190 195
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
 200 205 210
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
 215 220 225
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
 230 235 240
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
 245 250 255
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
 260 265 270
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
 275 280 285
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
 305 310 315
 Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
 320 325 330
 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
 335 340 345
 Ala Ala Arg Gly Pro Thr Ile Leu
 350

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
acctgcagag gaggcacatgac cccaaaccac catctcttta ctgtactagt 1000
cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100
atTTTTgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
 260

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
65 70 75

Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgctggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttgacca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

tgcacttata	tttttttagca	ctctgatcta	caaatttgga	agaaccgaag	600
agctatggac	ctgagatcac	ttcttaagtc	acatttttcct	tttgttatat	650
tctgtttgta	gataggtttt	ttatctctca	gtacacattg	ccaaatggag	700
tagattgtac	attaaatggt	ttgtttcttt	acattttttat	gttctgaggt	750
ttgaaatagt	tttatgaaat	ttctttatatt	ttcattgcat	agactgttaa	800
tatgtatata	atacaagact	atatgaattg	gataatgagt	atcagttttt	850
tattcctgag	atttagaact	tgatctactc	cctgagccag	ggttacatca	900
tcttgtcatt	ttagaagtaa	ccactcttgt	ctctctggct	gggcacggtg	950
gctcatgcct	gtaatcccag	cactttggga	ggccgaggcg	ggccgattgc	1000
ttgagggtcaa	gtgttttgaga	ccagcctggc	caacatggcg	aaaccccatc	1050
tactaaaaat	acaaaaatta	gccaggcatg	gtgggtgggtg	cctgtaatcc	1100
cagctacctg	ggaggctgag	gcaggagaat	cgcttgaacc	cgggggggcag	1150
aggttgcagt	gagctgagtt	tgcgccactg	cactctagcc	tggggggagaa	1200
agtgaaactc	cctctcaaaa	aaaagaccac	tctcagtatc	tctgattttct	1250
gaagatgtac	aaaaaaaatat	agcttcatat	atctggaatg	agcactgagc	1300
cataaaaggt	tttcagcaag	ttgtaactta	ttttggccta	aaaatgaggt	1350
tttttttgta	aagaaaaaat	atttgttctt	atgtattgaa	gaagtgtact	1400
tttatataat	gatttttttaa	atgccc aaag	gactagtttg	aaagcttctt	1450
ttaaaaagaa	ttcctctaata	atgactttat	gtgagaa		1487

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<210> 410
<211> 158
<212> PRT
<213> Homo sapiens
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<400> 410															
Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys	
1				5					10					15	
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala	
				20					25					30	
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	

[illegible]

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<210> 411
<211> 20
<212> DNA
<213> Artificial
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```
<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.
```

```
<400> 411
gtttgaggaa gctgggatac 20
```

```
<210> 412
<211> 20
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.
```

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<400> 412
      ccaaactcga gcacctgttc 20
```

```
<210> 413
<211> 40
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.
```

```
<400> 413
      atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40
```

<210> 414

[illegible]

383

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence

<210> 421
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 421
 gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1528
 <223> unknown base

<400> 422
 gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
 tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
 tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
 cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
 ctctctctct gctgtccta gtctcttagt cctcaaattc ccagtcccct 250
 gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300
 atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350
 acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
 cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
 ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
 ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
 tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
 cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
 tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
 atgacagctt gactgaggct gctgagaggc ctcagggcct ggctgtcctg 750
 ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
 tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

80	85	90
Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala	
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly	
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial


```
<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.
```

```
<400> 424
      gtaaagtcgc tggccagc 18
```

```
<210> 425
<211> 18
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.
```

```
<400> 425
cccgatctgc ctgctgta 18
```

```
<210> 426
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 426
ctgcactgta tggccattat tgtg 24
```

```
<210> 427
<211> 45
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.
```

```
<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45
```

```
<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens
```

```
<400> 428
aattttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacaqctca 150
```

```

aacctgcttt gggactccct ccacaaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350
gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgttcccggg aggcacacct 500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

```

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

```

<400> 429
Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
  1             5             10             15
Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
             20             25             30
Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
             35             40             45
Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
             50             55             60
Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
             65             70             75

```

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
80 85 90
Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
95 100 105
Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
110 115 120
Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
125 130 135
Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
140 145 150
Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
155 160 165
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
170 175 180
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
185 190 195
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
200 205

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

<400> 430
ggagagaggc gcgcgggtga aaggcgcatc gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgctctc gagatcccca aggggaagca 250
aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taattttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcacttaaata gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgtaagaat tttttttata tctgttaaata aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150
Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180
Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210
Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225
Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240
Leu Pro Lys

<210> 432
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 432
aggacttgcc ctcaggaa 18

<210> 433
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 433
cgcaggacag ttgtgaaaat a 21

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
atgacgctcg tccaaggcca c 21

<210> 435

1

```

<220>
<223> Synthetic oligonucleotide probe

<400> 440
    gggtcgtggtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
    ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
    tcctccatca ctccccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
    ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
    aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

```

<400> 445
 agcgtacact ctctccaggc aaccag 26

 <210> 446
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 446
 caattctgga tgaggtggta ga 22

 <210> 447
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 447
 caggactgag cgcttggtta 20

 <210> 448
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 448
 caaagcgcca agtaccggac c 21

 <210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 449
 ccagacctca gccaggaa 18

 <210> 450
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 450
 ccctagctga ccccttca 18

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456
ccttgaaaag gacccagttt 20

<210> 457
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457
atgagtcgca cctgctgttc cc 22

<210> 458
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458
tagcagctgc ccttggtta 18

<210> 459
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459
aacagcaggt gcgactcatc ta 22

<210> 460
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460
tgctaggcga cgacacccag acc 23

<210> 461
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

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<223> Synthetic oligonucleotide probe
<400> 461
    tggacacgtg gcagtgga 18
<210> 462
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 462
    tcatggtctc gtccattc 19
<210> 463
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 463
    caccatttgt ttctctgtct ccccatc 27
<210> 464
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 464
    ccggcatcct tggagtag 18
<210> 465
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 465
    tccccattag cacaggagta 20
<210> 466
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 466
```


<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 472
 tcagggtcta catcagcctc ctgc 24

 <210> 473
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 473
 aaggccaagg tgagtccat 19

 <210> 474
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 474
 cctactgagg agccctatgc 20

 <210> 475
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 475
 tccaggtgga cccacttca gg 22

 <210> 476
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 476
 gggaggctta taggccaat ctgg 24

 <210> 477
 <211> 50
 <212> DNA
 <213> Artificial Sequence

>
> Synthetic oligonucleotide probe

> 477

ttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50